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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Homo sapiens Eukaryote, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

Wands,J.R., de la Monte,S.M., Ince,N. and Carlson,R.I. Diagnosis and treatment of malignant neoplasms Patent: WO 0135102-A 3 17-MAY-2001; RHODE ISLAND HOSPITAL (US) Location/Qualiflers

.2324
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

source

ORIGIN

FEATURES

TITLE JOURNAL REFERENCE AUTHORS

			Description	AX146795 Sequence	S83325 aspartvl (as	CO871564 Sequence	U03109 Human aspar	M91213 Bos taurus	AF289486 Mus muscu	AF289487 Mus muscu	CO729666 Seguence	AF289489 Homo sapi				AR277619 Sequence	AR441744 Sequence	AR532049 Sequence	AX369081 Seguence		BC025236 Homo sapi	Mus
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DVWHPELTPQQRRSLPAI"
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1 (Dases 1 to 2324)
Lavaissiere, L., Jia, S., Nishiyama, M., de la Monte, S., Stern, A.M., Wande, J.R. and Friedman, P.A.

Overexpression of human aspartyl (asparaginyl) beta-hydroxylase in hepatocellular carcinoma and cholangiocarcinoma
J. Clin. Invest. 98 (6), 1313-1323 (1996)
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                                                                                                                                                                                                                                                                                       GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 179962] from the original journal article. Authors note differences between this sequence and that of F. Korioth. C. Gieffers, and J. Frey: Gene 150 (2), 395-399 (1994), GenBank U03109.
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    12. .2288
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/mol_type="maxwa"
/db_xref="taxon:9606"
1. 2324
2324
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S83325.1 GI:1911651
                                                                      Homo sapiens (human)
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g 8 셤 Seera, L.E.

Catarrhini, Hominidae; Homo.

Craniata; Vertebrata;

Chordata; Primates;

Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Mammalia; Eutheria;

1 Murphy, F.J., Sheehan, D.E., Keating, K.E., Hayes, I.E. and Enzymes involved in apoptosis Enzymes involved in apoptosis Patent: WO 2004078783-A 55 16-SEP-2004; Eirx Therapeutics Ltd (IE) Location/Qualifiers

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/mol_type="unassigned DNA"
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CQ871564 Sequence 55 from Patent CQ871564 CQ871564.1 GI:52745624

RESULT 3
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KEYWORDS

1927 AAAACCTGAGGGAAAAAGGGGACCTGGAGCCTGTTCACGCTGTGGCAGGAAGAAGAAGAAAACCTGTACTACTAGAAAAAGTTCCCCGAGA 1921 ATGAAAATGCCTGCAAAGGAGCTCCTAAAACCTGTACTAGTAGAAAAGTTCCCCGAGA 1987 ATGAAAAGTTCCCCGAAGAGAGCTCCTAAAACCTACTTACT	OY 1981 CARCAGANISCASANGASANGASANGASANGASANGASANGASANGASA	Oy 2101 AGGAAGGCTGCAAGATTCGATGTGCCAACGAGACCAGGACCTGGGAGGAAGGA		Oy 2281 CAATTTAGCATGAATTCATGCAAGCTTGGGAAACTCTGGAGAGA 2324	RESULT 4 HSU03109 LCCUS LCCUS LOCUS HSU03109 HSU03109 ASDETNITION Human aspartyl beta-hydroxylase mRNA, complete cds.	003109 003109.1 GI:458031 Homo sapiens (human)	Homo sapiens Eukaryota, Metazoa, Chordat. Mammalia, Eutheria, Primate 1 (bases 1 to 2249)	AUTHORS Korloth,F., Gleffers,C. and Frey,J. TITLE Cloning and characterization of the human gene encoding aspartyl beta-hydroxylase JOURNAL Gene 150 (2), 395-399 (1994)	TITLE Direct Submission JOURNAL Submitted (03-NOV-1993) Korioth F., Fakultaet fuer Chemie-Biochemie JI, Universitaet Bielefeld, Universitaetsstrasse 25, Bielefeld,	FEATURES Location/Qualifiers Source 12449 /organism="Homo sapiens"	/ db xref="texon:9606" /clone="As-5" /cell_line="mg63"	,	residues" /codon_start=1 /product="asparty1 beta-hydroxylase"	/protein_id="AAA82108.1" /db_xref="G1:458032" /translation="MAQRKNAKSSGNSSSSGSGSGSSSPGARRETKHGGHKNG
		CARA IGATUCARARCHARMAGCARANGTIVANGARARAGRAGCCIVARACITTITAARINAATT TIGATAAGACCTGTAAAGACGGAAAAA TIGATAAGACTGTTAAAGCTGAACTTGATGCTGCAGAAAAACTCCGTAAAAGGGGGAAAAA TIGATAAGACTGATGATGCTGAGAAAACTTGATGATGCTGAGAAAACTCCGTAAAAGGGGAAAAA	1081 TTGAGGAAGCAGTGATTTAAAGAACTAGTACGAAATACCTCAGAGTCCACGAG 1140	TGCTACGTGGAGCCATCGAGACCTACCAAGAGGTGGCCAGCCTACCTGATGTCCCTGCAG	TAGGTCATATGA	GAGGITCCCTGCTTACCCTGCAGAGATTAGTTCACTATTTCCCAGTGATTCTTTAA GAGGTTCCCTGCTTACCCTGCAGAGATTAGTTCAACTATTTCCCCAATGATACTTCCTTAA	ANAMATSACCIT GGCGTGGGGATACCT CTTGATGGGGGATAATGATGATGATGATGATGATTT TAAAATGACCTTGGGGGATACCTCTTGATGGGGGATAATGATGATGATGATGATGATGATGATG	ATGAAGGGTGCTGAGTGTGAGTGATGATGATGAGTTTGCTAAAGTCCATTATGGCTTCA ATGAAGGGTGCTGTGAGTGTGAAGGTTGATGATGGTTTGCTAAAGTCCATTATGGCTTCA	 1561 CCGGAGATCCTGGCACTGATGATGGGAGATTTTATTTCCACCTGGGGGATGCCATGCAGA 1620 	1621 GGGTTGGGAACAAAGAGGCATATAAGTGGTATGAGCTTGGGCACAAGAGAGACACTTTG 1680 	1681 CATCTGTCTGGCAACGCTCACTCTACAATGGACTGAAAGCACAGCCTTGGTGGA 1740 	1741 CCCCAAAAGAAACGGGCTACACAGAGTTAGTAAAGTCTTTAGAAAGAA	1801 TCCGAGATGAAGGCCTTGCAGTGATGGATAAAGCCAAAGGTCTCTTCCTGCCTG	1861 AAAACCTGAGGAAAAAGGGGACTGGAGCCAGTTCACGCTGTGGCAGCAAGAAGAAGAA 1920

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SCOCNQDWEEMASTGENDOSSEPVWEDERLHHDTDDVTYQVYEGQAVTEPLRYFWETTV
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RNEDVIKKALIKAELDAARKLARRACKIEBAVNAFKELDKRYFYPOSPRARYSKAQCEDDLAEKR
RSDTSLKNDLGVGYLLLGDVPADLLKLSLKSDRQQFLGHNGGSLLTLQRLVQLF
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PYLKEGIESGDPGTDGRFYPHLGDAMQRVGNKEAYRWYELGHRAGHPAVQNGSLIN
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2026 AGAACCTGAGGGAAAAGGGTGACTGGAGTCACTTTACGCTTG 1921 ATGAAAATGCCTGCAAAGGAGTCCCTAAAACCTGTACTTTAC 2086 ATGAAAATGCCTGCAAAGGAGCTCCTAAGACCTGTTCTTTAC 1981 CAACAGGATGCCGAAGAGGACCTCTAAGACTCTTTTTTTT	AF289486 Mus musculus aspartyl beta-hydroxylase 4.5 Mr289486 AF289486 AF289486 AF289486 GI:11878109 Mus musculus (house mouse) Mus musculus (house mouse) Mus musculus Gases 1 to 4419 Link,J., O'Neil,K.T., Focht,R.J., Sculry,M. Hollis,G.F. and Friedman,P.A. Dinnctin J. Box 1 to 4419) Dinctin 20564328 1095665 Losses 1 to 4419) Dinchuk,J.E., Henderson,N.L., Burn,T.C., Hor Friedman,P.A. Dincet Submission Submitted (26-JUL-2000) Applied Biotechnolc Submission Submitted (26-JUL-2000) Applied Biotechnolc Pharmaceuticals, P.O. Box 80400, Wilmington Location/Qualifiers 1. 4419 Acrain="BALB/C" Abox refe="taxon:10090" Abox refe="taxon:10000" Abox refe="taxon:10
bb 2026 Qy 1921 Db 2086 Qy 1981 Db 2146 Qy 2041 Db 2266 Qy 2161 Db 2266 Qy 2161 Db 2326 Qy 2221 Db 2346 Qy 2221	RESULT 6 AP289486 LOCUS DEFINITION ACCESSION VERSTON KEYNORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE FERTURES TITLE JOURNAL FEATURES SOURCE AUTHORS TITLE JOURNAL FEATURES SOURCE GENERAL FEATURES SOURCE GENERAL G

AUGCCTCATCTTCCGGCTGA 2220 AGCAGAGACGCAGCCTTCCAG 2280 linear ROD 18-DEC-2000 5 kb transcript (Asph) ACTAGAAAAGTTCCCCGAGA 1980 TGCACCCGGGACTCACGTGT 2040 ACCTGGGCTTGGTGATTCCCA 2100 GTGGCAGCAAGAAAAA 2085 ertebrata; Euteleostomi; i; Muridae; Murinae; Mus. evolutionarily conserved ain share exons with ology, DuPont con, DE 19880-0400, USA Huber, R., Ho, S.P., M.S., Hollis, J.M., Hollis, G.F. and

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                                                                                                                                                                                                                 note="BAH; asparaginyl beta-hydroxylase; AspH;
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strain="BALB/c"
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Mus musculus aspartyl beta-hydroxylase 6.6 kb transcript (Asph)
mRNA, complete cds; alternatively spliced.
AF289487.1 GI:11878111
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                           Eukarycia, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 6629)
Dinchuk, J. E., Henderson, N. L., Burn, T. C., Huber, R., Ho, S. P., Link, J., O'Neil, K. T., Focht, R. J., Scully, M. S., Hollis, J. M., Abpartyl beta - hydroxylase (Apph) and an evolutionarily conserved isoform of Asph missing the catalytic domain share exons with
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Direct Submission
Submitted (26-JUL-2000) Applied Biotechnology, DuPont Pharmaceuticals, P.O. Box 80400, Wilmington, DE 19880-0400, USA Location/Qualifiers
1. 6629
/ L. 6629
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AF289489 2680 bp mRNA linear PRI 18-DEC-2000 Homo sapiens aspartyl beta-hydroxylase 2.8 kb transcript mRNA, complete cds, alternatively spliced.
AF289489
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 2680)
Dinchuk, J.E., Henderson, N.L., Burn, T.C., Huber, R., Ho, S.P.,
Link, J., O'Neil, K.T., Focklr, R.J., Scully, M.S., Hollis, J.M.,
Hollis, G.F. and Friedman, P.A.
Aspartyl beta hydroxylase (Asph) and an evolutionarily conserved isoform of Asph missing the catalytic domain share exons with
                                                                                                                                                                                                                                                                                                                                                          1851 GATGACTCCTTTGAGCACGAGGTATGCCAGGATGCCTCATCCTTCCGGCTGATATTCATC
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                                                                             1551 AGGGAAAAAGGGGACTGGAGCCAGTTCACGCTGTGGCAGCAAGGAAGAAATGAAAT
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AGGGAAAAAGGGGACTGGAGCCAGTTCACGCTGTGGCAGCAAGGAAGAAGAAATGAAAAT
                                                                                                             GCCTGCAAAGGAGCTCCTAAAACCTGTACCTTACTAGAAAAGTTCCCCGAGACAACAGGA
                                                                                                                                                                   TGCAGAAGAGACAGATCAAATATTCCATCATGCACCCCGGGACTCACGTGTGGCCGCAC
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Dinchuk, J. F., Henderson, N. L., Burn, T. C., Hollis, G. F. and
Priedman, P. A.
Direct Submission
Submitted (26-JUL-2000) Applied Biotechnology, DuPont
Pharmaceuticals, P. O. Box 80400, Wilmington, DE 19880-0400,
Location/Qualifiers
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                                                                                                    Gaps
                                                                        Length 1970;
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                                                                       Score 1215.8; DB 6;
Pred. No. 7.5e-253;
0; Mismatches 141;
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                       Query Match 52.3%;
Best Local Similarity 90.2%;
Matches 1299; Conservative
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (Dasea 1 to 1080)

Strausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klaushara, C.M., Schuller, G.D., Altschul, S.F., Zeeberg, B., Eustow, K.H., Schaefer, C.F., Bhat, N. K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Mang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Devenshyuki, S., Carninci, P., Prange, C., Raba, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hullyk, S.W., Villadon, D.K., Gharathe, P.J., Horley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hullyk, S.W., Fahey, J., Halton, E. Ketteman, M., Wadan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Boutstand, G.G., Blakesley, R.W., Young, A.C., Shevchenko, Y., Bouterfield, Y. S., Krzywinski, M.I., Skalska, U., Schmutz, J., Worse, R.M., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
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On Aug 25, 2003 this sequence version replaced gi:15930166.
Contact: MGC help desk
Email: cgapbs.r@mail.nih.gov
Email: cgapbs.r@mail.nih.gov
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
ENNA Library Arrayed by: The I.M.A.G.E. Consortium (CLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (CLNL)
Enter Arrayed by: The I.M.A.G.E. Consortium (CLNL)
CONTACT: Stanford University School of Medicine, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                             1080 bp mRNA linear PRI 30-SEP-2003
Homo sapiens aspartate beta-hydroxylase, mRNA (cDNA clone
HMAGE:3887962), partial cds.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14589859.
Location/Qualifiers
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Strausberg, R.
Strausberg, R.
Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                  841 CAGAAGTAACTGCTCCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG
                                                            901 AAGTAAGCATTTTTCCTGTGGAAGAACAGCAGGAAGTACCACCAGAAACAAATAG 955
                                                                                                                                                                                      BC015518
BC015518.2 GI:34189304
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VERSION
KEYWORDS
SOURCE
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/product="asparty1 beta-hydroxylase 2.8 kb transcript"
/protein id="AAG40811.1"
/db_xrel="G1:11878116"
/db_xrel="G1:11878116"
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Pred. No. 1.5e-194;
0; Mismatches 5; Indels
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llarity 99.5%;
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CAGAAGTAACTGCTCCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG 1020
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                                                                                                                                                                                                                                                                CAGAAGTAACTGCTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG 900
                                                                                   CAGITICACAAGACIGIAAICAGGAIAIGGAAGAGAIGAIGICIGAGCAGGAAAAICCAG 720
                                                                                                                  -----CAG 840
                                                                                                                                               ATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCATGATACAGATGATGTAACAT 780
                                                      AGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGA 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2442)
Radosevich,J.A.
Gene encoding cancer marker labyrinthine
Patent: JP 2002512005-A 1 23-APR-2002;
JAMES A RADOSEVICH
JAMES A RADOSEVICH
C12N15/09, C07K14/47, C07K16/18, C12P21/08, C12Q1/02, C12Q1/68//
(C12P21/08, C12R1:91), C12N15/00
Gene encoding cancer marker labyrinthine
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                                                                                                                                                              AGCATGGAGGACACAAGAATGGGAAAAGGCGGGACTCTCGGGGAACTTCATTCTTCACGT
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Gene encoding cancer marker labyrinthine.
BD234762
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Pred. No. 8.4e-167;
0; Mismatches 10;
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    .2442
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

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Location/Qualifiers
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JP 2002512005-A/1
23-APR-2002
11-MAR-1999 US 09/040485
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98.8%;
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Homo sapiens (human)
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Best Local Similarity 98.8
Matches 825; Conservative
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AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
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KEYWORDS
SOURCE
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SEHVEGEDLQQBDGPTGEPQQEDDEFLMATDVDDRFETLEPBVSHEETEHSYHVBETD
SSERVVEDERLHHPTDDVTYQYYEEQAVYEPLENEGIEITEVTAPPEDNPVEDSQVIV
EEVSIPPVEEQQEVPPEKKKK
                                                                                                                                                                                                                                                                                                                                         /trānslation="MAQRKNAKSSGNSSSGSGSTSAGSSSPGARRETKHGGHKNG
RKGGLSGTSFFTWFMVIALLGVWTSVAVVWFDLVDYEEVLGKLGIYDADGDGDFDVDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1080;
                                                                                                                                                                             note="synonyms: JCTN, HAAH, CASQ2BP1, BAH"
                                                      /clone="IMAGE:3887962"
/tissue type="Lung, carcinoma, large cell
undifferentiated."
/clone lib="WIH MGC 69"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 829.6; DB 9;
Pred. No. 4.2e-169;
); Mismatches 4;
                                                                                                                                 note="Vector: pCMV-SPORT6
                                                                                                                                                                                                                                                                                  /protein_id="AAH15518.1"
/db_xref="GI:34189305"
                   organism="Homo sapiens"
                                                                                                                                                                                                                                                       'codon_start=1
'product="ASPH protein"
                                                                                                                                                                                                                                                                                                            /db_xref="LocusID:444"
/db_xref="MIM:600582"
                                                                                                                                                                                        /db_xref="LocusID:444'
/db_xref="MIM:600582"
189. .>1080
                                 'mol_type="mRNA"
'db xref="taxon:9606"
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/gene="ASPH"
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/gene="ASPH"
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                                                                                  GGTTTATGGTGATTGCATTGCTGGGCGTCTCGACATCTGTAGCTGTCGTTTGGTTTTAATC
                            TTGTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAG
                                                                                                                                                       CAGCAGTCCCGCCAGAAGAGGCTGAGCCACACAGTGAGCCCGAGGAGCAGGTTCCTGTGG
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1 (Dases I to 2442)

Wingy T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S., Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A. Compositions and methods for the therapy and diagnosis of lung
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Sequence 1791 from patent US 6509448.
AR277619.1 GI:29711268
    Mismatches
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1. 2442
/organism="unknown"
/mol_type="genomic DNA"
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/organism="unknown"
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Location/Qualifiers
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Unclassified.
1 (bases 1 to 2442)
3 Radosevich, J.
Gene encoding labyrinthin, a marker for cancer
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1 Location/Qualifiers
1 1 2442
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Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	67 AY405267 Homo sani	AY405268 Pan	AK030293 Mus	AK049506 M18	AK035735 Mus	AY405269 Mus	BM806632	BX403636	BX459083	AU130952	BU838423	CK724966	BM790814	BU166117	18 CD643948 AGENCOURT		BU190749 AGENCOURT	20 CN258120 170005325	BU502544	BU175716	CR630295	AW996828	CA317663	
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12 ATGGCCCAGCGTAAGAATGCCAAGAGCAGCAACAACAACAGCAGCAGCAGCGGCTCCGGCAGC 71

Query Match 88.4%; Score 2054.4; DB 9; Length 2126; Best Local Similarity 96.7%; Pred. No. 0; Matches 2055; Conservative 0; Mismatches 70; Indels 0;

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4.00 4.00	AY405267 Homo sapiens AS genomic survey AY405267 AY405267 GSS. GSS.	Bukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 2126) (Clark,A.G., Glanowsk Todd,M.A., Tanenbaum Ferriera,S., Wang,G. Adams,M.D. and Cargi Inferring nonneutral gene trios Science 302 (5652), (bases 1 to 2126)	Clark, A.G., G., Tad Todd, M.A., Tad Adams, M.D. and Direct Submiss Submitted (16 Rockville, MD This sequence them based on them based of the categories o
25 26 27 28 28 28 28 31 31 31 31 31 31 31 31 31 31	RESULT 1 AV40267 LOCUS DEFINITION ACCESSION VERSION VERSION CERYWORDS SOURCE ORGANISM		AUTHORS TITLE JOURNAL COMMENT FEATURES SOURCE gene

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1 ATGGCCCAGCGTAAGAATGCCAAGACCAGCGCAACAGCAGCAGCAGCGGCTCCGGCAGC 72 GGTAGCACGAGTGCGGCAGCAGCAGCCCGGGGCCGGAGAGAAACAAAGCATGGAGA 61 GGTAGCACGAGTGCGGGCAGCAGCCCCGGGGCCCGGAGAGACACAAAGCATGGAGGA 132 CACAAGAATGGGGGAAACTCTCGGGAACTTCATTCTTCACGTGGTTAATGGTG 121 CACAAGAATGGGAGAAAGCGGACTCTCGGGAACTTCTTCACGTGGTTTATGGTG 192 ATTGCATTGCTGGGAGAAAGGCGGACTCTCAGGAACTTCTTCACGTGGTTTATGGTG 193 ATTGCATTGCTGGGGCGTCTCGTAGCTGTTCTTCTTCACGTGTTGATCTTTTTTTT	Oy 252 GAGGAAGTICTAGGAAACTAGGAAICTATGAIGCTGAIGGAGAITITGAIGIG	432 CAGAATATCGAAGATGAAGACAAATTCAGTCCCTTCTCCATGAAATGGTACAC		732 CCAGTAGTAGAAGATGAAAGATTGCACCATGATACAGATGATAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGAAAGAAAGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAAATGAAAAATGAAAAAA	0y 852 GCTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAGAAGTAAGCATT Db	QY GAACAAAAAGCAAAAGTTAAGAAAAAGCCTAAACTTTTAAATAATTTGATAAGAT DD	OY 1092 GTGAATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAGTCCACGAGCAAGATAGGG

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961 GAAAAATTGAGGAAGCAGTGAATGCGTTTAAAGAACTAGTACGCAAATACCCCACAGAGTC 1020
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               GATITIGAGACCCIGGAACCIGAAGIAICTCAIGAAGAAACCGAGCAIAGIIACCACGIGG 654
                                                                                                                              715 ATCCAGATTCCAGTGAACCAGTAGAAGATGAAAGATTGCACCATGATACAGATGATG 774
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Direct Submission

L Submisted (16-NOV-203) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers

Location/Qualifiers

I. 2023

/organism="Pan troglodytes"
/mol type="genomic DNA"
/mol type="genomic DNA"
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Pan troglodytes ASPH gene, VIRTUAL TRANSCRIPT, partial sequence,
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B Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Inchani, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamira, M., Nishi, K., Nomura, K., Numaza, K., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saito, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sagabe, Y., Tanaka, T., Yasunishi, R., Numamatsu, M., Andria, S., Muramatsu, M., and Hayashizaki, Y., Yasunishi, A.,
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IQSILQESVHTDHDLEADGLAGEPQPEVEDFILTVTDSDDRFEDLEPGTVHEEIEDTYH
VEDTASQNHPNDMEEMTNEQENSDFSEAVTDAGVLLPHAEEVRHQDYDEPVYEFSEHE
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RKRGKIEEAVNAFEELVRKYPOSPARARYGRAQCEDDLARKORBNEVLERAIETVOBAA
DLPDAPTDLVKLSLKRRSERQOFLGHMRGSLLTLQRLVQLFPSDTTLKNDLGVSYLLL
GDNDSAKKYYEEVLLWTPNDGFAKVHYGFILKAQNKISESIPYLKGGIESGDPGTDDG
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ELVYSLERWWKLIRDEGLWWDKARGLFLPEDEDILEKRGHWSGPTLMOGGRKORDAC
KGAPKTCALLEKFSETTGCRRGJKYS IMHCTHVWPHTGPTNCRLERMILGLVYPKEG
CKIRCANETRTWEEGKVLIPDDSFEHEVWQDASSFRLIFIVDVWHPELTPQQRRSLPA
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(MGD|MGI:1914186, GB|NM_023066, evidence: BLASTN, 99%,
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AKHGGHKNGRRGGISGSSFFTWFMVIALLGVWTSVAVVWFDLVDYEEVLGKLGVYDAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Submiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
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                                                                                                                                                                                                                      Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                          Team and the
                                                                                                                                                                                     The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                            FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
                              RIKEN Genome Exploration Research Group Phase II
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URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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/db_xref="taxon:10090"
/clone="5031409C19"
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/proteIn_id="BAC26882.1"
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/strain="C57BL/6J"
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                                                               1741 AGGATGAAAACCTGAGGGAAAGAGGGGACTGGAGCCAGTTCACGCTGTGGCAGCAAGGAA 1800
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1675 ACTITGCATCTGTCTGGCAACGCTCACTCTACAATGTGAATGGACTGAAAGCACAGCCTT 1734
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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polyA_signal 43874392 /note="putative" polyA_site 4406 /note="putative"	Query Match 62.4%; Score 1450; DB 3; Length 4406; Best Local Similarity 79.4%; Pred. No. 0; Matches 1834; Conservative 0; Mismatches 380; Indels 96; Gaps 6;	15 GCCCAGCGTAAGAATGCCAAGAGCAGCGCAACAGCAGCAGCGGCTCCGGCAGCGGT 74	75 AGCACGAGTGCGGGCAGCAGCAGCAGCCCCGGGGCCCGGAGAGACAAAG 122 	123 CATGGAGGACACAAGAATGGGAGGAAAGGCGGACTCTCGGGAACTTCTTCATCTTCACGTGG 182 		GTTGACTATGAGGAAGTTCTAGGAAACTAGGAATCTATGATGCTGATGGTGATGGAGAT 	303 TTTGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAAGAGGAGATCTACTTCAGAGCCA 362 	GCAGTCCCGCCAGAAGAGGCTGAGCCACACACTGAGCCGGGGGGCAGGTTCCTGTG	GAGGCAGAACCCCAGAATATCGAAGATGAAGAAAAGAACAAATTCAGTCCCTTCTCCAT GAGGCAGAACTATCAAATATCGAAGAAGAAAAAAAAAA				ACACITICACAAGACIGIAAICAGGATAIGGAAGAGAIGAIGACGGAGGAAATICA 				GAAGTAAGCATTTTCCTGTGGAAGAACAGCAAGAAGAACACAAAAAAAA

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S. Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hiraokar, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komo, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Okazaki, Y., Satto, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Satto, R., Sattoh, H., Sakai, C., Sakai, K., Satzume, N., Sogabe, Y., Tangami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
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(MGD|MG1:1914186, GB|NM_023066, evidence: BLASTN, 99%,
match=4404)
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TGCRGGJIKYSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKEGCKIRCANETRTWEEGK
VLIFDDSFEHEVWQDASSFRLIFIVDVWHPELTPQQRRSLPAI"
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/db_xref="raxon:10090"
/db_xref="raxon:10090"
/clone="C430018B11"
/tissue type="whole body"
/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="7 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Parploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1.7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCCCCCGGGCCCCGGAGAGACAAG 122
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Please visit our web site for further details.
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/db_xref="G1:26340240"
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URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
1..3924
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 AGCACGAGTGCGGGCAGCAGC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2334 AIAITCATCGTGGATGTGTGGCACCCCGAGCTGACCCCTCAGCAGAGACGCAGCCTTCCC 2393
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Mus musculus 7 days embryo whole body cDNA, RIKEN full-length enriched library, clone:C430018B11

product:aspartate-beta-hydroxylase, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCATCTTTGATGACTCTTTTGAGCACGAGGTTTGGCAGGATGCCTCGTCTTTCCGGCTG 2333
                                                                                                                                                                                                                                                                                            Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                      TGGCCGCACACAGGGCCCACAAACTGCAGGCTCCGAATGCACCTGGGCTTGGTGATTCCC
                                                                                                                                                                                                                 AAGGAAGGCTGCAAGATTCGATGTGCCAACGAGACCAGGAACGCAAGGCAAGGTG
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High-efficiency full-length CDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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HTC; CAP trapper.
Mus musculus (house mouse)
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS TITLE JOURNAL MEDLINE

PUBMED AUTHORS

REFERENCE

REFERENCE

REFERENCE AUTHORS MEDLINE PUBMED

JOURNAL

TITLE

PUBMED REFERENCE AUTHORS

JOURNAL

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TITLE JOURNAL REFERENCE AUTHORS

JOURNAL

TITLE

DEFINITION

RESULT 4 AK049506

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/protein id="BAC29171.1"
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/bcrtein id="RG1:26330882"
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HTDHDLEADGLAGEPQPEVEDFLITVIDESDRFEBLEFETHYEETEDFYHTEDTASQNH
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HYGFILKAQNKISESIPYLKEGIESGDPGTDDGRFYPHLGDAMQRVGNKEAYKMYELG
HKRGHFASVWQRSLYNVNGLKAQPWWTPRETGYTELVKSLERNWKLIRDBGLMVMDKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="unnamed protein product; aspartate-beta-hydroxylase (MGD|MGI:1914186, GB|NM_023066, evidence: BLASTN, 99%, match=4404)
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BQQDTPPVKKKKKPKILINKFDKT I KAELDAAEKLRKRGKI EEAVNAFEELVRKY PQSPR
ARYGKAQCEDDLAEKQRSNEVI.RRA I ETYQEAADLPDAPTDI VKLSI.KRRSERQQFLG
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YSIMHPGTHVWPHTGPTNCRLRMHLGLVIPKBGCKIRCANETRTWEEGKVLIFDDSFB
HEVWQDASSFRLIFIVDVWHPELTPQQRRSLPAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="urinary bladder"
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dev_stage="adult"
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                                                                                                                                 in Riken
                                                                                                     cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGACAAAGCATGGAGGACACAAGAATGGGAGGAAAGGCGGACTCTCGGGAACTTCATTC
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                   Kanagawa 230-0045, Japan (E-mail:genome-reeggsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
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Location/Qualifiers
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/db_xref="taxon:10090"
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                                                         AK035735

Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530097J16
product:aspartate-beta-hydroxylase, full insert sequence.
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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CTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGATTGCAACAAGAAGAT [ACCAGAAACA ACC ACCTAAACTT SCCTAAACTT	962 CTGAACAAATTTGATAAGACAATTAAGGCTGGGATGCTGCAGAAAGCTCCGGAAA 1021 1071 AGGGAAAAATTTGAGAAGCAGTGAATGCATTTAAAGAACTAGTAACGCAAATAACCCTCGG 1130 1022 AGGGGAAAAATTGAGGAAGGAGTGATGCATTTAAAGAACTAGTTCGAAAGTACCCTCAG 1130 1131 AGTCCACGAGAAGATTAAGGAAAGCAGCAGTTTAGAGAATTGGTTCGAAAGTACCCTCAG 1081 1082 AGCCCACGAGACAAGATATGGCAAGAGCAGCAGTGTAGAGATGATTTGGCTGAGAAGAGAGAG	1251 GTCCCTGCAGACCTGAAGCTGAGTTTGAAGCGTCAGACAGCAACAATTTCTA 1310	1431 AAGAAAGTTATGAAGAGGGCCGAGGGCCCCCAATGACGAGAGAGGCCCCCCCC

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       Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Lu, F., Murphy, B., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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                                                                                        925 AACAGCAGGAAGTACCACCAGAAACAAATAGAAAAACAGATGATCCAGAACAAAAAGCAA
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E 1 (Mages 1 to 1050)
S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Lupublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ArcC.CoTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Libri at:
http://inage.llni.gov
Plate: Libralizes row: k column: 24
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CCAGTTCACGCTGTGGCAGCAAGGAAGAAATGAAAATGCCTGCAAAGGAGCTCCTAA 1948
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Homo sapiens
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Outcact: Genoscope
Contact: Genoscope
Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoXV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
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Catarrhini, Hominidae, Homo.
                                                                                                 721 ATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCATGATACAGATGATGTAACAT
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                               590 AAATGNTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCAACAG
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                                                                              541 GAGAACCACAACAAGAGGATGATTTTTTTTTTTTGCCGACTGATGTAGATGATTTTG
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This sequence belongs to sequence cluster 4537.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CSODE012CA07QP1&c=4537.r.
Location/Qualifiers
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Verte
Eukaryota; Metazoa; Chordata; Catarrhini; Hom
Mammalia; Eutheria; Primates; Catarrhini; Hom
In (bases 1 to 1085)
Lil, W.B., Gruber, C., Jessee, J. and Polayes, D.
Unpublished (2001)
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double-strand cDNA was digested with Not I and cloned into
Library was not normalized."
                                                                                                                                                                                                                                                               Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
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division of Invitrogen.
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                                                                  Vertebrata; Euteleostomi;
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For more information about this cluster, see
http://www.genscope.cns.fr/cdna?e=CLOBA0072C04RP1&c=4537.r.
Location/Qualifiers
                                                                                                                                                                                       On May 13, 2003 this sequence version replaced gi:30635043.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
                                                                  Craniata, Vertebrata, Eutele
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llarity 97.6%; Pred. No. 9.9e-213;
Conservative 5; Mismatches 17; Indels 0;
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Mammalia, Butheria, Primates, Catarrhini, Hon
1 (bases 1 to 1011)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Will-length cDNA libraries and normalization
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Isogai,T.

Harl human cDNA project

Unpublished (2000)

Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute
T512-3 Yana, Kisarazu, Chiba 292-0812, Japan
T61: 81-438-52-3986

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Email: genomicsOhri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                       ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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the Not I and EcoRV sites of the pCMVSPORT 6 vector Library was not normalized."
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                                                       Length 1085;
                                                                                 Indels
                                                     Score 834.6; DB 5;
Pred. No. 9.3e-203;
1; Mismatches 5;
                                                     35.9%;
ilarity 99.3%;
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837; Conserv
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CK724966 182 bp mRNA linear EST 05-AUG-2004
UI-H-ED1-axp-c-22-0-UI.s1 NCI_CGAP_ED1 Homo sapiens cDNA clone
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S'-GACTAGTTCTAGATCGCGAGCCGCCCT(15)-3'. Size selected : 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAGITITCACAAGACTGTIATCACGAIATGGAATAGATGATGATGATGATGATGATGAAAATCCA
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                                                                                                                                   930;
                                                                                                                                   Length
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                                                                                                                                Match 31.0%; Score 719.8; DB 5; Local Similarity 96.3%; Pred. No. 2.7e-173; les 758; Conservative 0; Mismatches 27;
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
E 1 (Gases 1 to 930)
I Gases 1 to 930)
INTH-MCC http://mgc.nci.nih.gov/.
INTH-MCC http://mgc.nci.nih.gov/.
Insulished (1999)
I Unpublished (1999)
I Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CONTACT: Robert Straved by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
http://image.llnl.gov f column: 15
High quality sequence stop: 549.
I Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                               GAAGTTAATCCGAGATGAAGGCCTTGCAGTGATGGATAAAGCCAAAGGTCTCTTCCTGCC 1852
                                                                                                                                                      CATGCAGAGGGTTGGGAACAAAGAGGCCATATAAGTGGTATGAGCTTGGGCACAAAGAGAGG 1672
                                                                                                                                                                                                                                                                                 /clone lib="Lupski dorsal root_ganglion"
/note="Vector: pcMV-SPORT6 (Life Technologies); Site_1:
Not1; Site_2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
                                           ACACTTIGCATCTGTCTGGCAACGCTCACTCTACAATGTGAATGGACTGAAAGCACAGCC
                          AATAGAATCCGGAGATCCTGGCACTGATGATGGGAGATTTTTATTTCCACCTGGGGGATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="dorsal root ganglia"
/dev stage="adult, 36 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l. .930
organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6177038"
                                                                                                                                                                                                                                                                                                                                                                                                                TGAGGATGAAACCTGAGGGAAAA 1876
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Homo sapiens
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KEYWORDS
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AUTHORS
TITLE
JOURNAL
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CTGGCACTGATGATGGGAGATTTTATTTCCACCTGGGGGATGCCATGCAGAGGGTTGGGA 1629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM790814 689 bp mRNA linear EST 05-MAR-2002
K-EST0070696 S21SNU520 Homo sapiens CDNA clone S21SNU520-16-C08 5',
mRNA sequence.
BM790814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryogram, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Kim.N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Kim,Y.S., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

Ele Frontier Korean EST Project 2001

Contact: Kim YS
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                                                      TGCTGAGTGTGACACCTAATGATGGCTTTGCTAAAGTCCATTATGGCTTCATCCTGAAGG
                                                                                                                                                                                                                                              357 CIGGCACTGATGAGAGATTTTATTTCCACCTGGGGGATGCCATGCAGAGGGTTGGGA
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Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
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/cell_type="Floating aggregates"
/cell_line="SNU-520"
/lab_nost="ToplOF"
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="$218NU520-16-C08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 16 row. C column: 08
High quality sequence stop: 689.
Location/Qualifiers
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Homo sapiens
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                                                                                                                                                                                                                        Tumor Gene Index Cancer, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)

Unpublished (1997)

Office of Cancer Genomics
National Cancer Institute / NIH

Bldg: 31 RmlOAO7 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html

Seq primer: M13 FORWARD

POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.../W2

// Organism="Homo sapiens"
// Mol type="mRNA"
// Mol type="mRNA"
// Mol type="mRNA"
// Lissue_type="Chondrosarcoma"
// Lissue_type="Chondrosarcoma containing the following tissue(s): Chondrosarcoma cell
// Site 2: Not I: NOI CGAP_EDI is a normalized CDNA library
// Containing the following tissue(s): Chondrosarcoma cell
// Site 2: Not I: NOI CGAP_EDI is a normalized cDNA library
// Containing the following tissue(s): Chondrosarcoma cell
// Site 2: Not I: NOI CGAP_EDI is a normalized oble servent of some Research, 6:791-806,
// Oligo-dT primer containing a NoI I site. Double stranded
cDNA was ligated to an ECOR I adaptor, digested with Not
// Signouclectide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
// CISSUE-chondrosarcoma
// TAG_INSUE-chondrosarcoma
// TAG_INSUE-chondrosarcoma
// TAG_INSUE-chondrosarcoma
// TAG_INSUE-chondrosarcoma
// TAG_INSUE-chondrosarcoma
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                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dasses 1 to 782)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 697; DB 7; Length 78:
Pred. No. 1.9e-167;
0; Mismatches 7; Indels
UI-H-ED1-axp-c-22-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cocation/Qualifiers
                  CK724966
CK724966.1 GI:42535838
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Best Local Similarity 98.9%;
Matches 709; Conservative (
                                                                                  sapiens (human)
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/Glone IlD="SLISNUSIGN"
// CLONE ILD="SLISNUSIGN"
// CLONE ILD="SLISNUSIGN"
// Site 2: Not1; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intext mRNA was ligated with DNA-RNA linker including ECOR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The CDNA vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coll DNA ligase after digestion of
ECORI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
converted colls E. coll TOPAlly this method are
the cDNA libraries constructed by this method are
full-length enriched cDNA library."
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                                                                                                                                                                                                                                                                                                                                                                                   29.6%; Score 689; DB 4; Length 68 larity 100.0%; Pred. No. 2e-165; Conservative 0; Mismatches 0; Indels
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Matches 689; Conserv
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   918 bp mRNA linear EST 04-SEP-2002
_7914661 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6147375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:6147375"
/tissue type="melanotic melanoma"
/tissue type="melanotic melanoma"
/tissue type="melanotic melanoma"
/clone lib="NHH MGC 72"
/note="Organ: 8kin; Vector: pCMV-SPORT6; Site 1: Not1;
/ste 2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 918)
NHH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LlAM13477 row: b column: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 918;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 667.8; DB 5;
Pred. No. 6.2e-160;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 634.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                     BU166117.1 GI:22680069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.7%;
Local Similarity 91.3%;
les 775; Conservative
                                                                                                  Homo sapiens (human)
                                   5', mRNA sequence.
BU166117
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                             AGENCOURT,
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Bukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bi (bases 1 to 765)

NIH-MGC http://gec.nci.nih.gov/.

NIH-MGC http://gec.nci.nih.gov/.

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

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National Cancer Ensitute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapps-r@mil.nih.gov

Tissue Procurement: Irene Ginis and Mahendra Rao, NIA

CDNA Library Preparation: Yulan Piao and Minoru Ko

CDNA Library Arrayed by: Man I.N.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC c

Can be found through the I.N.A.G.E. Consortium/LLNL at:

Plate: NDANSII row: a column: 24

High quality sequence stop: 605.
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AGENCOURT_14550808 NIA Human H1 Embryonic Stem Cell cDNA Library
Liong) Homo sapiens CDNA clone IMAGE:30425975 5', mRNA sequence.
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/uncte="Vector: pCMV-Sport6; Site 1: Not1; Site 2: Sal1; /note="Vector: pCMV-Sport6; Site 1: Not1; Site 2: Sal1; This is a long-transcript enriched CDMA library (Genome Res. 11: 1553-1558 (2001). [PMID: 11544199] From WA01 cell line . Undifferentiated human ES cell line WA01 was obtained from Wichall Research Institute, Inc., Madison, Wi, cultured according to their instructions on MEF feeders. They formed round colonies with defined edges and were positive for alkaline phosphatase, SERA-4, OCT3, OCT4, REX1, OTF, TERT, SOX2, CX43 and CX45. They are negative for GATA2, GRA4, PDX1, NCAM, MSX1, FLT3, SEBA-1, TUBB3, NES, GFAP, and EOMES. When confluent (18-10 days after plating), the ES cells from 4 X cm dishes were treated with 1 mg/ml collegenase, type IV (Invircogen/GIECO) for 5-10 min and gently scraped off with 5 ml pipette. RNA was purified with TRIZOl Reagent from Invitrogen. Protocol ref. Genome Res. 11: 1553-1558 (2001). [PMID:11544199]) Double-stranded CDNAs were synthesized with an Oligo(dT) primer [Invitrogen: Strands with an oligo(dT) primer [Invitrogen: Column Then, the CDNAs were amplified by lethanol-precipitation. The CDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-s for 25 cycles. The products were purified by phenol/chloroform extraction and column. The CDNAs were amplified by mare purified by phenol/chloroform extraction and separated from extraction and centricon-100 column. The cDNAs were digested with Sal and Not! enzymes and cloned into Sal1/Not1 site of about 3.6kb."
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28.3%; Score 657.6; DB 6; Length 765; 97.6%; Pred. No. 2.4e-157; live 0; Mismatches 16; Indels 1 Local Similarity 97.6 es 677; Conservative Query Match Best Loca Matches

Gaps

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TGAAGGGATAGAAATCACAGAAGTAACTGCTCCCCTGAGGATAATCCTGTAGAAGATTC 883

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ACAGGTAATTGTAGAAGAAGTAAGCATTTTTCCTGTGGAAGAACAGCAGGAAGTACCACC

Search completed: March 25, 2005, 14:28:59 Job time : 6791 secs

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March 24, 2005, 12:41:52 ; Search time 1157 Seconds
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polypeptides are hydroxylated by HAAH enzymes. HAAH is used in the method of the invention. The specification describes a method for diagnosing a malignant neoplasm in a mammal. The method comprises contacting a body fluid with an antibody which binds to HAAH polypeptide under complex forming conditions, and detecting the antigen-antibody complex. The method is useful for diagnosing and prognosing a malignant neoplasm in a bodily fluid e.g. central nervous system (CNS) derived body fluid, blood, serum, urine, saliva, sputum, lung effusion, and ascites fluid of mammal, where the neoplasm is derived from endodermal tissue and is selected from colon cancer, breast cancer, pancreatic cancer, liver cancer, cancer of bile ducts, and cancer cancer in the deal of the colon cancer for the CNS. HAAH antibodies, linked to a cytotoxic agent, are useful for killing tumour cells
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                                                                                                                                                                                             2221 TATTCATCGTGGATGTGTGGCATCCGGAACTGACACCAGCAGCAGCAGCAGCCTTCCAG 2280
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, 89; gene; aspartyl (asparaginyl) beta-hydoxylase; HAAH; cytostatic; immunostiant; antibody; neoplaem; timmour; FB50; 86A; 5C7; 198; brain tumour; glioma; glioblastoma; astrocytoma; haemangioma; pancreatic carcinoma; colon cancer; braast cancer; pancreatic carcinoma; rolon cancer; braast cancer; pancreatic cancer; liver cancer; cancer of the bile ducts; primary malignant CNS neoplasm; metastatic CNS neoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing neoplasm and inhibiting tumor growth, by contacting tissue of
                                                                                                                                   AGGAAGGCTGCAAGATTCGATGTGCCAACGAGACCAGGACTTGGGAGGAAGGTGC
ATGAAAATGCCTGCAAAGGAGCTCCTAAAACCTGTACCTTACTAGAAAGTTCCCCGAGA
           GGCCGCACACAGGCCCCACAAACTGCAGGCTCCGAATGCACCTGGGCTTGGTGATTCCCA
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                                            CAACAGGATGCAGAAGAGACAGATCAAATATTCCATCATGCACCCCGGGACTCACGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA encoding aspartyl (asparaginyl) beta-hydoxylase, HAAH.
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(DMON/) DE LA MONTE S M.
(DEUT/) DEUTCH A H.
(GHAN/) GHANBARI H A.
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The invention relates to diagnosing a neoplasm and inhibiting tumour growth in a mammal, using an antibody that binds to human aspartyl carparaginyl) beta-hydroxylase (HAAH). Diagnosing a neoplasm comprises in level of antibody binding at tissue site compared to the level of an increase in level of antibody binding at tissue site compared to the level of a monoplasm at the tissue site. Inhibiting tumour growth in mammal involves deministering the antibody conjugated to a cytcoxic agent to a mammal. Involves administering the antibody conjugated to a cytcoxic agent to a mammal. In a mammal involves and included are a method of conferring an immune response to a tumour cell in a mammal party administering to the mammal and propertied (or a polymuclectied composition encoding the antibody or an HAAH polypeptide, or its degenerate variant), a fragment of HAAH, and the polypeptide (or a polymuclectied composition encoding the polypeptide, or its degenerate variant), a fragment of HAAH, and the polypeptide, or its degenerate variant, and expensive the antibody is FBSO, and a fragment of HAAH (where the antibody is FBSO, 66A, 5C7 or 19B) a hybridoma cell line chosen from hybridoma PBBO, HA386A, HA1SCA and HA219B, and a fragment of HAAH which lacks enzymatic activity or alpha-ketoglutarate binding domain and each astrocytoma cell and HAAH-specific immune cesponse to a brain tumour growth in a mammal, conferring an immune cervicatic carcinoma cell and for inducing a HAAH-specific immune response to a mammal, for conferring immune response to a paracteric carcinoma cell and for inducing a HAAH-specific immune response in a mammal. How cancer, pancreatic carcinoma cell and for inducing a HAAH-specific immune ceponse in a mammal that or conferring immune response to a carcinoma cell and for inducing encert and cancer, pancreatic carcinoma cell and for inducing encert and cancer, pancreatic carcinoma cell and for inducing encert and cancer, pancreatic carcinoma manal conferring a useful for diagnosing nephame cell origin an
          human aspartyl
nammal with detectably-labeled antibody which binds to (asparaginyl) beta-hydroxylase.
                                                                                        Example 1; Page 4-5; 34pp; English.
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Sequence 2324 BP; 753 A; 463 C; 625 G; 483 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a method for inhibiting tumour growth in a mammal. The method comprises administering to the mammal a compound, which inhibits the expression or enzymatic activity of a human aspartyl (asparaginyl) beta-hydroxylase (HAAH). The compound may inhibit HAAH hydroxylation of a NOTCH polypeptide. In particular, the compound may inhibit hydroxylation of an epidermal growth factor (EGF)-like repeat sequence in a NOTCH polypeptide. The methods are useful for inhibiting tumour growth or killing tumour cells, or for diagnosing or prognosticating a mallignant neoplasm. In particular, the tumour or neoplasm is colon cancer, breast cancer, pancreatic cancer, liver cancer, grace of the bile ducts, or cancer or tumour of the central nervous system (CNS). The present sequence encodes HAAH.
                                                                                                                                                                                                                                                                            Inhibiting tumor growth or killing tumor cells (e.g. cancer of the colon, breast, pancreatic, liver or the central nervous system), by administering an inhibitor of the human aspartyl (asparaginyl) betahydroxylase.
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immunosuppressive; osteopathic; antidiabetic; dermatological;
antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;
                                                                                                  PRO polypeptide encoding cDNA SEQ ID NO:1092.
                        BP
                       standard; cDNA; 2452
                                                                              (first entry)
                                                                            18-NOV-2004
                                                  ADP23914;
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The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has polypeptide encoded by it. A protein of the invention has polypeptide encoded by it. A protein of the invention has antiarthritic, antialatergic, and propertied is useful for treating an immune related disorder such as systemic lupus erthritis, a spondyloarthropathy, systemic solerosis, antidopathic inflammatory myopathy. Slogren's syndrome, systemic clupus erthritis, a sarcoidosis, autoimmune haemolytic anaemia, autoimmune disease, a demyelinating disease mellitus, immune-mediated renal disease, a demyelinating polymeuropathy, antialateral nervous construction inflammatory demyelinating polymeuropathy, a hepatobilary disease, infectious or autoimmune chronic active hepatitis, primary cirrhosis, granulomacous hepatitis, sclerosing chood inflammatory demyelinating polymeuropathy, whipple's bilary cirrhosis, granulomacous hepatitis, sclerosing chood infecase, arthoma multiforme, contact dermatitis, psoriasis, an altergic chimitis, acopic dermatitis, gooriasis, an allergic chimitis, acopic dermatitis, grantly hypersensitivity, urticaria, an immunologic disease of the lung, hypersensitivity, urticaria, an immunologic disease of the lung, hypersensitivity, articaria, an immunologic disease, grade menteropathy content demonitis, a transplantation associated diseases, grade menteropathy content demonit
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gene therapy; immune system.
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AGCATGGAGGACACAAGAATGGGAGGAGAAAGGCGGACTCCTCAGGAACTTCATTCTTCACGT
                                                                   GGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC
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     GAGGTTCCCTGCTTACCTTGCAGAGATTAGTTCAACTATTTCCCCAATGATACTTCCTTAA
                            CCGGAGATCCTGGCACTGATGATGATGGAGATTTTATTTCCACCTGGGGGATGCCATGCAGA
                                                                                                                                   GGGTTGGGAACAAAGAGGCATATAAGTGGTATGAGCTTGGGCACAAAGAGAGGACACTTTG
                                                                                                                                                        CATCTGTCTGCCAACGCTCACTCTACAATGTGAATGGACAGGAACGCCTTGGTCGA
                                                                                                                                                               ATGAAAATGCCTGCAAAGGAGCTCCTAAAACCTGTACCTTACTAGAAAAGTTCCCCGAGA
                                                                                                                                                                                                                                                      CAACAGGATGCAGAAGAGACAGATCAAATATTCCATGATGCACCCCGGGACTCACGTGT
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This invention relates to novel isolated cDNAs that are differentially expressed in MYCN activated cells. Specifically, it refers to compressed in MYCN activated cells. Specifically, it refers to protected sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a protectly and anoters. The present invention describes these componing sneeds. The present invention describes these componing to a useful for in hybridisation assays to detect expression of nucleic acids for complementary nucleic acids) in a present in a given sample, as specifically bind the cDNA as a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also that is differentially expressed in MYCN activated cells, given in an exemplification but has been obtained in electronic format from the US petent Office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the
                                                                                                                                                                                63
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                                                                                                                                                             Bovine cDNA differentially expressed in MYCN activated cells SeqID
                                                                                                                                                                                                                     bovine; differential expression; transactivator; proto-oncogene; neuroblastoma; small cell lung cancer; cytostatic; gene therapy; MYCN activated cell.
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99.8%; Score 2319.2;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2321; Conservative 0; Mismatches
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ADJ56257 standard; cDNA; 5358
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                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stuart SG, Nuchtern JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (STUA/) STUART S G.
(NUCH/) NUCHTERN J G.
(PLON/) PLON S E.
(SHOH/) SHOHET J M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-635698/60.
                                                                                                                                                                                                                                                                                                                                                                                         JS2003119009-A1.
                                                                                                              06-MAY-2004
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                                                        ADJ56257;
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The invention relates to new isolated nucleic acid molecule comprising a nucleic acid molecule consisting of a gene differentially expressed in cells undergoing differentiation from mesenchymal cell to a cells undergoing differentiation from mesenchymal cell to a chondroblastic phenotype, or hybridising under stringent conditions to them (or their fragments). Also included are expression vectors, transformed host cells, expressed polypeptides or peptide fragments of minimogen). binding partners of the polypeptides or peptide fragments of identifying an agent useful in modulating mesenchymal cell and may be used as an immogen). binding partners of the polypeptides, a method for differentiation induction activity of a molecule, a method of diagnosing a condition characterized by aberrant expression of a nucleic acid molecule or its expression product, a method for determining regression, progression or onset of cartilaginous tissue degeneration condition, a method for treating a subject to reduce the cisk of cartilaginous tissue degeneration condition, and a solid-phase nucleic condition, and acid molecule array consisting essentially of a set of nucleic acid molecule array consisting essentially of a set of nucleic acid differentially expressed in developing mesenchymal cells using the celliferentially expressed in developing mesenchymal cells using the conditions and agents and agents and agents are useful for treating cartilaginous tissue of degeneration conditions and agent arthritis, rheumatoid arthritis, deptherm and solvant arthritis, arthritis deformans, infectious conditions and agent arthritis, arthritis deformans, infectious and agent arthritis, arthritis deformans, infectious and submarchymal cells are submarchymal cells arthritis arthritis, actually expressed in developing mesenchymal cells arthritis actually expressed in developing mesenchymal cells arthritis, adjuvant arthritis arthritis deforment in developing mesenchymal cells arthritis arthritis arthritis arthritis arthritis arthritis arthritis 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecules capable of promoting chondrogenesis, useful for diagnosing and treating cartilaginous tissue degeneration conditions, e.g. offeoarthritis, rheumatoid arthritis, gout arthritis, or
                                                                                                                                                                                                                                                                                                       Human, 88; gene; skeletal growth; cartilage degeneration disorder; chondroblastic phenotype; mesenchymal cell; cartilage formation; bone formation; arthritis; osteoarthritis; rheumatoid arthritis; gout arthritis; adjuvant arthritis; arthritis; arthritis; arthritis; osteochondrosis; RDA; antiarthritic; osteopathic; antirheumatic; antiinflammatory; representational difference analysis.
                                                                                                                                                                                                                                                           Human mRNA differentially expressed in mesenchymal cells #25.
2538 CAATTTAGCATGAATTCATGCAAGCTTGGGAAACTCTGGAGAGA 2581
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                                                                                                                    ABX04178 standard; cDNA; 2680 BP
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                                                                                                                                                                                                                (first entry)
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                                                                                                                                                  AGCATGGAGGACACAAGAATGGGAAGAAAAGGCGGACTCTCGGGAACTTCATTCTTCACGT
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                       Length 2680;
Sequence 2680 BP; 854 A; 446 C; 575 G; 805 T; 0 U; 0 Other;
                     Score 947; DB 6; Length 26
Pred. No. 8.8e-220;
0; Mismatches 5; Indels
                 Query Match
Best Local Similarity 99.5%;
Matches 950; Conservative
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RESULT 8 ADP24208

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The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has polypeptide encoded by it. A protein of the invention has antidiabletic, dermatological, antipsoriatic, antidiabletic, dermatological, phones to propertide is useful for treating an immune related disorder such as agonist, antagonist, or antibody that specifically binds to the agonist, antidiamly related an immune related disorder such as pystemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, or systemic sclerosis, andiopathic inflammatory myopathy, Sjogren's syndrome, systemic sclerosis, antidimmatory myopathy, Sjogren's syndrome, thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal crossorial interval and polymeuropathy, Guillain-Barre syndrome, system, idiopathic demyelinating polymeuropathy, Guillain-Barre syndrome, system, idiopathic demyelinating polymeuropathy, Guillain-Barre syndrome, confisease, infectious or autoimmune chronic active hepatitis, primary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Mulple's clisease, asthma, allergic rhinitis, atopic dermatitis, food disease, asthma, allergic rhinitis, atopic dermatitis, protein or pneumonitis, a transplantation associated disease, graft rejection or consumption or immunologicalisease, draft rejection or consumptions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral
                                                                                                                                                  ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2680 BP; 854 A; 446 C; 575 G; 805 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van Lookeren M, Williams PM,
                                                                                                              polypeptide encoding cDNA SEQ ID NO:1386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1386; 2940pp; English.
standard; cDNA; 2680 BP
                                                                                                                                                                                                                                                                                                                                                                                30-OCT-2003; 2003WO-US034312
                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-2002; 2002US-0423394P
                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2004-419628/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; ADP24209
                                                                                                                                                                                                                                                                                                     WO2004041170-A2.
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                                                                                                                                                                                                                                                               Unidentified
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                                                                               18-NOV-2004
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      ADP24208
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                                                                                          TTGTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAG
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                                           AGCATGGAGGACACAAGAATGGGAGAAAAGGCGGACTCTCGGGAACTTCATTCTTCACGT
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GGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC
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Score 947; DB 13; Length 2680; Pred. No. 8.8e-220;); Mismatches 5; Indels 0

CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCAGCGGCAACAGCAGCAGCAGCA

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Best Local Similarity 99.5 Matches 950; Conservative

Similarity

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541 GAGAACCACAACAAGAGGATGATGAGTTTCTTATGGCGACTGATGTAGATGATAGATTTG 600
         AGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG
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                                                                                                        AAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCAACAG
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08-SEP-2000; 2000US-00658124.

26-SEP-2000; 2000US-00671325.

06-OCT-2000; 2000US-00677419.

30-OCT-2000; 2000US-0073457.

13-DEC-2000; 2000US-00734657.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel polynucleotide and polypeptide sequence for the antigen detected by the antibody MCA 44-3A6. This antigen is designated Labyrinhin (lab). Antibodies directed to the Labyrinhin (lab) accepted to the Labyrinhin (lab) antibodies directed to the Labyrinhin (lab) brotein are useful for the detection of Lab. The Lab protein is amount of antibodies (this method is especially useful for accer and that have the Lab marker). As the Lab gene is not tissue-specific, it will detect cancer regardless of which organ it occurs in. Peptides cancers and/or to treat humans with cancer. Antibody MCA 44-1A6 is able to differentiate antigens associated with adenocarcinomas. However, the cancers and/or to treat humans with cancer. Antibody MCA 44-1A6 is able to differentiate antigens associated with adenocarcinomas. However, the cancer control of the antigen detected by this antibody as not been elucidated sequence of this antigen would enhance its usefulness in cancer diagnosis, treatment and prevention. The present invention discloses the sequences of the antigen recognized by the MCA 44-3A6 antibody. This sequence of the antigen recognized by the MCA 44-3A6 antibody. This sequence of the antigen recognized by the MCA 44-3A6 antibody. This sequence of the antigen recognized by the MCA 44-3A6 antibody. This sequence of the antigen recognized by the MCA 44-3A6 antibody. This sequence of the numan lab protein described in the method of the
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            Labyrinthin; human; cancer; marker; antigen; detection; antibody; MCA 44-3A6; diagnostic; vaccine; treatment; adenocarcinoma; ds.
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Pred. No. 1.2e-188;
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Best Local Similarity 98.8%;
Matches 825; Conservative (
                                                                                                                                                                                                                                                             (RADO/) RADOSEVICH J A.
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P-PSDB; AAY33642.
                                                                                                                                                                                                                                                                                          Radosevich JA;
                                                        Homo sapiens.
                                                                                                                                                   WO9947683-A1
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ACA12072 standard; cDNA; 2442
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FANGER G R.
WANG A.
SWITZER A P.
MCNEILL P D.
CLAPPER J D.
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P-PSDB; ABU69516.
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                                                                                                             The invention describes an isolated polynuclectide and polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the polynuclectide and/or polypeptide is useful for treating a lung cancer in a patient. The polypeptide is useful for removing tumour cells from a biological sample. The polynuclectide is useful for removing tumour probe or primer to detect the level of mRNA encoding a tumour protein. This sequence encodes a lung tumour associated protein or protein. Fragment, described in the method of the invention. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                         Novel polynucleotide encoding a lung tumor polypeptide useful for stimulating and/or expanding T cells specific for a tumor protein
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  c GR, Vedvick TS, Bangur
Mcneill PD, Clapper JD;
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                                                                                                                                                                                                                                                                                              35.2%; Score 819; DB 6; L 98.8%; Pred. No. 1.2e-188; iive 0; Mismatches 10;
                                                                                             Claim 7; SEQ ID NO 1791; 223pp; English.
      Fanger
                Wang A, Fanger N, Switzer A,
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 98.8
Matches 825; Conservative
      Carter D,
                                      WPI; 2002-164634/21.
      Marnerakis M,
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The invention relates to a polynucleotide encoding a lung tumour protein, comprising a sequence selected from any of the 14 sequences mentioned in comprising a sequence selected from any of the 14 sequences mentioned in specification, or a sequence (S2) mentioned in specification, complement of S1, sequences to S1, sequences to complement of S1, sequences that hybridise to S1, sequences having 75%, preferably of S1, sequences that hybridise to S1, sequence from any one of isolated polypeptide (comprising a sequence (S1) selected from any one of isolated polypeptide (comprising a sequence shaving at least 70%, concerned by the polynucleotide, or sequences having at least 70%, conferably 90% identity to a sequence encoded by the polynucleotide, and sequence compression control sequence, a host cell transformed or transfected with expression control sequence, a host cell transformed or transfected with the vector, an isolated antibody (or its antigen-binding fragment) that the vector, a final prince to the polypeptide, detecting the presence of a cancer conficically binds to the polypeptide, detecting the presence of a cancer in a patient, a fusion protein comprising the polypeptide, an oligonucleotide that hybridises to S1 under moderately stringent conditions, stimulating and/or expanding T cells specific for a tumour
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                                                                                                                                                                                                                                    784
                                                                      724
                                                      CAGAAGTAACTGCTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG
ACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAAAATGAAGGGATAGAAATCA
                                                                                                                                                                                                                                                                                                                   901 AAGTAAGCATTITICCTGTGGAAGAACAGCAGGAAGTACCACCAGAAACAAATAG 955
                                                                                                                                                                                                                                                                                                                                                         Mcneill PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human lung cancer-associated cDNA L979P extended sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; lung cancer; ss; lung tumour; cytostatic; vaccine; T cell expansion; CD4; CD8.
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us-09-436-184-3.rng

724 900

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correcting comparising contacting T cells with the polynuclectide, protein correcting cells, under conditions and for a time sufficient content and the standard content of T cells) and inhibiting the development of a cancer in a patient (by incubating CD4+ and/or CD8+ T cells isolated from a patient with the polynuclectide, protein or antigen presenting cells that express the polynuclectide, such that T cells presenting cells, and thus inhibiting the development of the conformation of a cancer in the patient. The polynuclectide, protein and scills are useful in a composition for stimulating an immune response in a patient, and for composition for stimulating an immune response in a patient, and for compositions are useful in paramacentical compositions, e.g. vaccines. The polynuclectide are useful in paramacentical compositions, e.g. vaccines. The polynuclectide is also useful as a probe or patient. The protein and oligonuclectides are useful in pharmacentical compositions, e.g. vaccines. The polynuclectide is also useful as a probe or primer for nucleic acid hybridisation, and in the design and proteins in tunour cells. An amplified portion of tunour polynuclectide is useful for isolating a full length excended or ibrary. The present sequence is a cDNA (full length gene from a suitable planary. The present sequence is a cDNA (full length excended or conformatial) isolated from a library derived from lung tunour/cancer cells. Sequence data for this patent did not form part of the printed conformatial in eaguence. The present did not form part of the printed conformatial in electronic format directly from the sequence.
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The invention describes an isolated polynucleotide comprising one of 32 sequences, complement or degenerate variants of them. The polynucleotide is useful for preparing a composition e.g. a vaccine or for gene therapy, for treating or inhibiting development of cancer, e.g. lung cancer. This sequence represents a polynucleotide associated with the compositions and methods for the therapy and diagnosis of lung cancer
              CAGAAGTAACTGCTCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide, useful for preparing a composition for treating or inhibiting development of cancer, e.g. lung cancer.
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Mcnabb A;
                                                                                                                                                                                                                                                                      Lung cancer; cytostatic; vaccine; gene therapy; cancer; gene;
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Durham M, Carter D, Fanger GR, Vedvick TS, Bangur CS,
                                                                                                                                                                                                                                                 Lung cancer therapyand diagnosis associated cDNA #1745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; SEQID NO 1791; 82pp; English.
                                                                                                                                                                            ACA03258 standard; cDNA; 2442 BP.
                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-1999; 99US-00346492.
15-OCT-1999; 99US-00419356.
17-DEC-1999; 99US-00419356.
30-DEC-1999; 99US-00476687.
22-MAR-2000; 2000US-00519642.
22-MAR-2000; 2000US-0051964.
27-APR-2000; 2000US-00519184.
27-APR-2000; 2000US-00519184.
27-APR-2000; 2000US-00561184.
28-AUG-2000; 2000US-005182.
28-EEP-2000; 2000US-005182.
28-EEP-2000; 2000US-005182.
30-CCT-2000; 2000US-0057132.
30-CCT-2000; 2000US-0057132.
31-DEC-2000; 2000US-0057132.
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                                                                                       TTGTTGACTATGAGGAAGTTCTAGGAAACTAGGAATCTATGATGCTGATGGTGATGGAG
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                                                          GGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC
                            AAGTAAGCATTTTCCTGTGGAAGAACAGCAGGAAGTACCACCAGAAAAAAAG 955
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Length 2442;
               10; Indels
Score 819; DB 8; I
Pred. No. 1.2e-188;
0; Mismatches 10;
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98.8%;
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The invention relates to novel compositions and methods for the therapy and diagnosis of cancer, particularly lung cancer. The compositions comprise one or more lung tumour polypeptides, immunogenic portions thereof, polynocleorides that encode such polypeptides, antigen presenting cells that express such polypeptides, and T cells that are specific for cells expressing such polypeptides. The novel compositions have cycostatic and immunostimulant activity. The lung tumour antigens can be used in the creation of a vaccine. The polynucleotides that encode the lung tumour polypeptides can be used in gene therapy to help in the treatment of lung tumours. This polynucleotide sequence represents a treatment of lung tumours. This polynucleotide sequence represents a human lung tumour cDNA clone of the invention. This sequence was not human lung tumour cDNA clone of the invention. This sequence was not broperty Organization CD ROM supplied with the specification.

Seguence 2442 BP; 781 A; 391 C; 512 G; 758 T; 0 U; 0 Other;

Vedvick TS

Sleath PR; Fanger GR,

ο, υ,

Kalos N Carter I

Watanabe Y, Durham M,

Henderson RA, Wang T, I Johnson JC, Retter MW, Johnson JC, Retter M Bangur CS, Mcnabb A; WPI; 2003-468346/44.

(CORI-) CORIXA CORP.

28-OCT-2002; 2002WO-US034777. 29-OCT-2001; 2001US-00017754.28-MAR-2002; 2002US-00113872

WO2003037267-A2 sapiens

Homo

08-MAY-2003

New polypeptides and encoding polynucleotides, useful for diagnosing, preventing and/or treating lung cancer.

Example 5; SEQ ID NO 1791; 258pp; English.

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AGGCAGAACCCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCTTCTCCATG 480
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                                                                                                                                                                                                                                                                                                         aaatggtacacgcagaacatgttgagggagaacatgcaacaagagagatggacccacag
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                                                                                                   ATTITGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAAGAGAGATCTACTTCAGAGC
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                                                       GGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC
                                          121 AGCATGGAGGACACAAGAATGGGAAGAAAGCGGACTCTCGGGAACTTCATTCTTCACGT
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35.2%; Score 819; DB 10; Length 2442; 98.8%; Pred. No. 1.2e-188; inde 0; Mismatches 10; Indels 0.
      Query Match 35.2
Best Local Similarity 98.8
Matches 825; Conservative
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lung cancer; tumour; cytostatic; immunostimulant; vaccine; gene therapy; human; clone; ss.

Human lung tumour cDNA clone, SEQ ID No 1791

(first entry)

25-MAR-2004

ADH47310;

ADH47310 standard; cDNA; 2442

RESULT 13

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The invention relates to a novel isolated polynucleotide comprising a sequence chosen from any one of 40 lung tumour polypeptides or its complements, fragments or degenerate variants. The method of the invention has cytostatic applications and may be useful for detecting and treating lung cancer in a patient, as well as for inhibiting the development of lung cancer in a patient via incubating Cut+ and/or CD8+ rolls isolated from a patient with at least one component chosen from a polypeptide, polynucleotide or antigen presenting cell (AFC) of the invention and administering an effective amount of the proliferated T cells to the patient. The current sequence is that of the human lung cancer-related CDNA of the invention. The current sequence is not shown in the specification per se but is available on the USPTO web-site http:seqdata.uspto.gov/sequence.html?DocID=20030211510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 GGTITATGGTGATTGCTGGGGCGTCTGGACATCTGTAGCTTGGTTTGATC 124
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                    Vedvick TS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.2%; Score 819; DB 13; Length 2442; 98.8%; Pred. No. 1.2e-188; ive 0; Mismatches 10; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2442 BP; 781 A; 391 C; 512 G; 758 T; 0 U; 0 Other;
                    Fanger GR,
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                 Carter
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                 Durham M,
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             Retter MW,
Mcnabb A;
                                                                     WPI; 2004-167010/16.
P-PSDB; ADJ21244.
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               Johnson JC,
Bangur CS,
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                    AGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAA
                                                                                                  CAGTITCACAAGACTGTAATCAGGATATGGAAGAGATGATGTCTGAGCAGGAAAATCCAG
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15-OCT-1999; 99US-00419356.
17-DEC-1999; 99US-0046867.
06-MAR-2000; 2000US-00519642.
22-MAR-2000; 2000US-00519642.
10-APR-2000; 2000US-00546259.
10-APR-2000; 2000US-00546259.
55-JUN-2000; 2000US-0056046.
55-JUN-2000; 2000US-00561184.
11-JUL-2000; 2000US-00561154.
29-AUG-2000; 2000US-00561154.
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06-OCT-2000; 2000US-00674419.
30-OCT-2000; 2000US-0070S705.
13-DEC-2000; 2000US-00736457.
03-MAX-2001; 2001US-00849626.
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New human protein modification and maintenance molecules (PMMM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMMM expression e.g. cancer, atherosclerosis, or
ATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCATGATACAGATGATGTAACAT 664
                           840
                                                  ACCAAGTCTATGAGGAACCAAGCAGTATATGAACCTCTAGAAAATGAAGGGATAGAAATGA 724
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                                                                                                                                                                                                                                                                                                                                        Human, protein modification and maintenance molecule, PWMM, cancer; cell proliferation disorder; atherosclerosis, neurological disorder; epilepsy; Huntington's disease; stroke; immune disorder; allergy; inflammatory disorder; AIDS; developmental disorder; hypothyroidism; cushing's syndrome; gastrointestinal disorder; hypothyroidism; inflection; cytostatic, antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiallergic; vulnerary; antiinflammatory; thyromimetic; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ramkumar J, Gorvad AE, Baughn MR, Emerling BM, Yang J, Lee SY; Tran UK, Becha SD, Duggan BM, Lee EA, Griffin JA, Li JX; Spraque WM, Hafalia AJA, Chawla NK, Lehr-Mason PM, Kable AE, Yue Marquis JP, Yao MG, Richardeon TW, Tang TY, Jin P, Chien D; Pharia U, Burrill JD, Lee S, Blake JJ, Ho A, Zheng W;
                                                                                CAGNAGTAACTGCTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG
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                                                                                                                                     Claim 5; Page 306; 311pp; English.
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25-OCT-2001; 2001US-0335703P.
09-NOV-2001; 2001US-0348887P.
28-NOV-2001; 2001US-0334145P.
06-DBC-2001; 2001US-0337451P.
14-DEC-2001; 2001US-0340584P.
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                                                                                                                                                                                                                                                                                                                      human PMMM-33
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The present invention relates to the isolation of human protein modification and maintenance molecules (PMMM), and the polymucleotide sequences encoding them. A total of 40 PMMM polypeptides (designated PMMM -1 to PMMM-40) are disclosed. The sequences of the invention are useful for diagnosing a condition or disease associated with the expression of PMMM in a subject, preparing a polyclonal or monoclonal antibody, and

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generating an expression profile of a sample containing the polynucleotides. The diseases or conditions associated with decreased expression or overexpression of Phym are cell proliferation disorders (e.g. cancer, atheroscletosis), neurological disorders (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory disorders, (e.g. AIDS, allergies), developmental disorders (e.g. hypothyroidism, Cushing's allergies), gastrointestinal or epithelial disorders, and infections. The Phym polypeptides or their fragments are useful in screening compounds for effectiveness as agonists or antagonists of the polypeptides, or in altering the expression of the target polynucleotide and compounds specifically bind to, or modulate the activity of the polypeptide. ACA92416-ACA92455 encode the human PWMM polypeptides of the invention
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9	2324	100.0		6	US-09-903-023-3	Sequence 3, Appli
7	2324	100.0		10	US-09-436-184-3	Sequence 3, Appli
60	2319.2	99.8		15	US-10-084-817-63	Sequence 63, Appl
0	947	40.7		16	US-10-096-534-37	Sequence 37, Appl
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	RESULT 2 US-09-859-604-3 ; Sequence 3, Application US/09859604	Patent No. US2020110559A1 GENERAL INFORMATION: APPLICANT: Wands, Jack R.	; APPLICANT: de la Monte, Suzanne M ; APPLICANT: Deutch, Alan H ; APPLICANT: Ghanbari, Hossein A ; TITLE OF INVENTION: DIAGMOSIS AND TREATMENT OF WALIGNANT NEOPLASMS	FILE REFERENCE: 21486-032 CIP CURRENT APPLICATION NUMBER: US/09/859,604 CURRENT FILING DATE: 2001-05-17 PRIOR APPLICATION NUMBER: 09/436.184	; PRIOR FILING DATE: 1999-11-08 ; NUMBER OF SEQ ID NOS: 13 ; SCOFTWARE: PatentIn Ver. 2.1 ; SEO ID NO 3	ro.	Query Match 100.0%; Score 2324; DB 9; Length 2324; Best Local Similarity 100.0%; Pred. No. 0; O. 0 Matches 2324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	GGGCAACAGCAGCAG	Qy 61 GCTCCGGCAGCGGTAGCACGACGAGCAGCAGCCCGGGAGCCCGGAGAGACAA 120 Db 61 GCTCCGGCAGCGGTAGCACGAGCAGCAGCAGCCCCGGGAGAGACAA 120	CATTCTTCACGT	TTTGGTTTGATC	Qy 241 TIGTIGACTAIGAGGAAGTICTAGGAAACTAGGAATCTAIGATGCTGATGGAGGGGG 300	QY 301 ATTITGATGIGGATGATGCCAAAGTITTATTAGGACTITAAAGAGAGATCTACTICAGAGC 360 Db 301 ATTITGATGIGGATGATGCCAAAGTITTATTAGGACTTAAAGAGAGATCTACTICAGAGC 360	Qy 361 CAGCAGTCCCGCCAGAAGAGGCTGAGGCCCCGAGGAGCAGGTTCCTGTGG 420. Db 361 CAGCAGTCCCGCCAGAGAGGCTGAGCCCACACACTGAGCCCCGAGGACCAGGTTCCTGTGG 420.		ATGGACCCACAG	Qy 541 GAGAACCACAACAAGAGGATGATGATTCTTATGGCGACTGATGTAGATGATAGATTTG 600 Db 541 GAGAACCACAACAAGAGGATGATGTTTTTTTTTTTTTTT	Oy 601 AGACCCTGGAACCTGAAGTATCTGATGAAGAAACCGAGGATTACCACGTGGAAGAGA 660

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APPLICANT: Shazon E. Plon
APPLICANT: Jed G. Nuchtern
APPLICANT: Shazon E. Plon
APPLICANT: Gason M. Shohet
TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
FILE REFERENCE: PA-0046 US
CURRENT APPLICATION NUMBER: US/10/084,817
CURRENT FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 60/270,784
PRIOR APPLICATION NUMBER: 60/270,784
SPRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 365
SOFTWARE: PERL PROGram
SEQ ID NOS: 365
                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CRGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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US-10-084-817-63
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Pred. No. 0;
0; Mismatches
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US-10-084-817-63
Sequence 63, Application US/10084817
Publication No. US20030119009A1
GENERAL INFORMATION:
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Best Local Similarity 99.5%;
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9 720 180 480 540 540 900 900 120 TIGITGACTATGAGGAAGTICTAGGAAACTAGGAATCTATGATGCTGATGGAGG 300 ATTITGATGATGATGCCAAAGTTTATTAGGACTTAAAGAGAGATCTACTTCAGAGC 360 360 420 420 480 180 240 120 9 9 CAGTITCACAAGACTGTAATCAGGATATGGAAGATGATGTCTGAGCAGGAAAATCCAG CAGCAGTCCCGCCAGAAGAGGCTGAGCCACACTGAGCCCGAGGAGCAGGTTCCTGTGG AGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGA AGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAAACAAATTCAGTCCCTTCTCCATG 481 AAATGGTACACGCAGAACATGTTGAGGAGAGAGACTTGCAACAAGAAGATGGACCCACAG 1 CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCGGCGAACAGCAGCAGCG 61 ecrecegoracidade a consequencidade a conseque GGTTTATGGTGATTGCATTGCTGGCGTCTGGACATCTGTAGCTGTGGTTTGGTTTGATC 121 AGCATGGAGGACACAAGAATGGGAGGAAAAGGCGGACTCTCGGGAACTTCATTCTTCAGT Gaps Sequence 3, Application US/10269909;
publication No. US20030180747A1
GENERAL INFORMATION:
APPLICANT: HAUBAN, RALPH H.
APPLICANT: HACGOUZIO-DONAHUE, CHRISTINE
APPLICANT: MATTRA, ANIBBAN
TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES
FILE REFERENCE: \$8303/71699)
CURRENT FILING DATE: 2003-10-11
PRIOR APPLICATION NUMBER: US/10/269,909
CURRENT FILING DATE: 2001-10-11
PRIOR FILING DATE: 2001-10-11
PRIOR FILING DATE: 2001-10-11
PRIOR FILING DATE: 2001-10-11
SIGN NUMBER OF SEQ ID NOS: 87
SOFTWARE: PARENT OF SEQ ID NOS: 87
SOFTWARE: DAA
SOFTWARE: HOMO 33
LENGTH: 2680
TYPE: DNA
SOGANISM: Homo sapiens ö Length 2680; 5; Indels Query Match
Best Local Similarity 99.5%; Pred. No. 1.3e-214;
Matches 950; Conservative 0; Mismatches 5; 661 ઠે

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        305 AGGCAGAACCCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG 364
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                                                           AAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCACAG
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APPLICANT: Watanabe, Yoshiniro
APPLICANT: Watanabe, Yoshiniro
APPLICANT: Watanabe, Yoshiniro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Marnerakis, Margarita
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Gary R.
APPLICANT: Monab, Andriany S.
APPLICANT: Monab, Andriany S.
APPLICANT: Monab, Andriany S.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121, 478617
CURRENT APPLICATION NUMBER: US/09/902, 941
CURRENT APPLICATION NUMBER: US/09/902, 941
SOFTWARE: FREE SECO IO WASS. 2002
SOFTWARE: FREE SECO IO WASS. 2002
SECO ID NO 1791
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Best Local Similarity 98.8%; Pred. No. 3.7e-184;
Matches 825; Conservative 0; Mismatches 10; Indels
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Patent No. US20020172952A1
GENERAL INFORMATION:
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US-09-902-941-1791
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                               ATTCCAGTGAACCAGTAGAAGATGAAAGATTGCACCATGATACAGATGTAACAT
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                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GREATCANT: MANGY, TONGEONG
APPLICANT: BANGE, Michael A.
APPLICANT: LOGGE, Michael A.
APPLICANT: LOGGE, Michael A.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE OF INVENTION: LIGAM
TITLE OF INVENTION: LIGAM
TITLE OF INVENTION: LIGAM
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT APPLICATION NUMBER: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
NUMBER OF SEQ ID NOS: 1864
                                                                                                                                                                                                                                                                                                                              Sequence 1791, Application US/09736457
Patent No. US20020168637A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-736-457-1791
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                                   Length 2442,
                                                       10; Indels
                                    35.2%; Score 819; DB 9; 1
98.8%; Pred. No. 3.7e-184;
iive 0; Mismatches 10;
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Publication No. US20030054363A1
GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
                                       Query Match
Best Local Similarity 98.8
Matches 825; Conservative
          sapiens
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US-10-017-754-1791
        , ORGANISM: HOMO
US-09-849-626-1791
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                              TTGTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAG
                                          CAGCAGICCCGCCAGAAGAGGCTGAGCCACACTGAGCCCGAGGAGCAGGTTCCTGTGG
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AAGTAAGGATTTTTCCTGTGGAAGAACAGCAGGAAGTACCACCAGAAACAATAG 955
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Sequence 1791, Application US/09849626
Publication No. US20020197669A1
GENERAL INFORMATION:
APPLICANT: Banger, Chaitanya
APPLICANT: Banger, Gary
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Walg, Tongtong
APPLICANT: Witzer, Anne
APPLICANT: McNeill, Patricia
APPLICANT: McNeill, Patricia
APPLICANT: Clapper, Jonachan
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION UNMBER: US/09/849,626
CURRENT APPLICATION NUMBER: US/09/849,626
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 1926
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1791
LENGTH: 2442
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US-09-849-626-1791
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               301 ATTITGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAAGAGAGATCTACTTCAGAGC
                       245 CAGCAGTCCCGCCAGAAGAGGCTGAGCCACACACACAGAGCCCGAGAGCAGGTTCCTGTGG
                                                                                 CAGCAGTCCCGCCAGAAGAGGCTGAGCCAACACTGAGCCCGAGGAGCAGGTTCCTGTGG
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us-09-436-184-3.rnpb

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301 ATTITGATGIGGATGATGCCAAAGITITATTAGGACTTAAAGAGAGATCTACTTCAGAGC 360
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                 CAGAAGTAACTGCTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG
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                                                                                                                                                                   RESULT 15
US-10-113-872-1791
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Best Local Similarity 98.8%; Pred. No. 3.7e-184;
Matches 825; Conservative 0; Mismatches 10; Indels
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Reter, Marca W.
APPLICANT: Marnerakis, Margarita
APPLICANT: Marnerakis, Margarita
APPLICANT: Carter, Darrick
APPLICANT: Panger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Workick, Thomas S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE BERERENCE: 210121.478618
CURRENT APPLICATION NUMBER: US/10/017,754
CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SOFTWARE: FREESEQ for Windows Version 4.0
LENGTH: 2442
                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-017-754-1791
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Search completed: March 25, 2005, 17:33:28 Job time : 1237 secs

Sequence 193, App Sequence 191, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 187, App Sequence 6, App 11 Sequence 6, App 11 Sequence 1318, App Sequence 12345, Sequence 12345, Sequence 12345, Sequence 1, App 11 Sequence 2, App 11 Sequence 3, App 11 Sequence 4, App 11 Sequence 2, App 11 Sequence 3, App 11 Sequence 4, App 11 Sequence

US-09-461-697-193 US-09-461-697-191 US-09-461-697-189 US-09-461-697-185 US-09-461-697-185 US-09-461-697-185 US-09-949-016-15770 US-09-357-014-8 US-09-357-014-8 US-09-357-014-6 US-09-357-014-6 US-09-357-014-6 US-09-357-014-6 US-09-357-014-6 US-09-357-014-6 US-09-357-014-6 US-09-373-462-2 US-09-973-462-1 US-09-973-462-1 US-09-973-462-1 US-09-973-462-1 US-09-973-462-1 US-09-973-462-1 US-09-248-796A-972-1

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Parent No. 6783758

GENERAL INFORMATION:

APPLICANT: Wands, Jack R.

APPLICANT: Ac la Monte, Suzanne M.

APPLICANT: Ince, Nedim

APPLICANT: Carlson, Rolf I.

TILLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REFERENCE: 2.1486-03.2 DIVS

CURRENT APPLICATION NUMBER: US/09/903,248

CURRENT PLICATION NUMBER: 09/436,184

PRIOR APPLICATION NUMBER: 09/436,184

PRIOR FILING DATE: 1999-11-08

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 2324; DB 4; Length 2324; Best Local Similarity 100.0%; Pred. No. 0; Marches 2324; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Homo sapiens
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-705-1791

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US-09-671-325-1791

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US-09-671-325-1791

US-09-671-325-1791

US-09-949-016-1889

US-09-949-016-12387

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US-09-192-116-11

US-08-179-116-12

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                 TTGAGGAAGCAGTGAATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAGTCCACGAG
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PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 2324
                                                                                    Query Match
Best Local Similarity 100.0%;
Matches 2324; Conservative 0;
                                                      TYPE: DNA
ORGANISM: Homo sapiens
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AGGTCATATGA 1320 ... ||||||||||| |GGTCATATGA 1320 LAGGGGAAAAA 1080 |||||||||||| AGGGGAAAAA 1080 JAGTCCACGAG 1140 |||||||||| JAGTCCACGAG 1140 AGTAATGAGG 1200 ||||||||||| AGTAATGAGG 1200 rgrccrgcag 1260 ||||||||||| rgrccrgcag 1260 TTAAATAAAT 1020 |||||||||||| TTAAATAAAT 1020 AATAGAAAA 960 |||||||||| AATAGAAAA 960 AAGAAAGTTT 1440 CGATGTAACAT 780 |||||||||||| |CATGTAACAT 780 GAAAATCCAG 720 ||||||||||| |GAAATCCAG 720 ATAGAAATCA 840 |||||||||||| |ATAGAAATCA 840 GGACCCACAG 540 |||||||||| |GGACCCACAG 540 GTGGAAGAGA 660 |||||||||||| GTGGAAGAGA 660 ACTTCAGAGC 360 |||||||||| ACTTCAGAGC 360

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   ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF FILE REPERENCE: 21466-032 DIV3
; CURRENT APPLICATION NUMBER: US/09/903,063
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PATENTIN VET. 2.1
; SEQ ID NO 3
                                                                                                        Query Match
100.0%; Score 2324;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2324; Conservative 0; Mismatches
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Patent No. 6815415
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
APPLICANT: de la Wonte, Suzanne M.
APPLICANT: Ince, Nedim
APPLICANT: Carlson, Rolf I.
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Carter, Darrick
APPLICANT: Vedvick, Tom
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Pan, Liqun
APPLICANT: Pa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-702-705-1791

; Sequence 1791, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
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Best Local Similarity 98.8
Matches 825; Conservative
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ORGANISM: Homo sapiens
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US-09-702-705-1791
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                     ENCODING A NOVEL MARKER FOR
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/040,485

FILING DATE: 17-MAR.1998

CLASSIFICATION: 530

ATTORNBY AGENT INFORMATION:

NAME: Martin, Alice O.

REGISTRATION NUMBER: 8998/3

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTER STICS:

LYPE: MUCLeic acid

STRANDEDNESS: single
                TITLE OF INVENTION: A GENE ENCODING A NOVEL MARKER TITLE OF INVENTION: CANCER NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS: ADDRESSEE: RENINKS, HOFER, GILSON & LIONE STREET: NBC Tower - Suite 3600, 455 N. Cityfront STREET: Plaza Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.4%; Score 823.8; DB 3;
llarity 99.2%; Pred. No. 6.8e-226;
Conservative 0; Mismatches 7;
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Best Local Similarity
Matches 828; Conserv
                                                                                                                                                                                    CITY: Chicago
STATE: Illinois
COUNTRY: USA
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LOCATION:
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US-09-671-325-1791

// Sequence 1791, Application US/09671325

// Patent No. 6667154

// GENERAL INFORMATION:
// APPLICANT: Wang, Tongtong
// APPLICANT: Lodes, Michael A.
// APPLICANT: Fanger, Gary
// APPLICANT: Penger, Gary
// APPLICANT: Retter, Darrick
// APPLICANT: Retter, Darrick
// APPLICANT: Retter, Marc
// APPLICANT: Retter, Ma
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; Patent No. 650948
; Patent No. 650948
; GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Panger, Gary
; APPLICANT: Retter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Retter, Marc
; APPLICANT: Retter, Marc
; APPLICANT: Fanger, Marc
; TITLE OF INVENTION: COMPOSITIONS FOR LUNG CANCER
; TITLE PERERROF: 2010.11-13
; TITLE OF INVENTION WINBER: US/09/736,457
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SEQ ID NO 1791
; LENGTH: 2442
; TYPE: DAR
; ORGANISM: Home Bapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 35.2%; Score 819; DB 4; Length 2442; Best Local Similarity 98.8%; Pred. No. 1.6e-224; Matches 825; Conservative 0; Mismatches 10; Indels
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                                                                                                             Length 2442;
                                                                                                                                  10; Indels
                                                                                                              Score 819; DB 4; L
Pred. No. 1.6e-224;
0; Mismatches 10;
 DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANC FILE REFERENCE: 210121.478C12
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1791
LENGTH: 2442
                                                                                                                35.2%;
nilarity 98.8%;
Conservative 0
                                                                            TYPE: DNA
CRGANISM: Homo sapiens
US-09-671-325-1791
                                                                                                                            Similarity
                                                                                                                            Best Local Similaring Matches 825;
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                                       GENERAL INFORMATION:
APPLICANT: RADOSEVICH, JAMES A.
TITLE OF INVENTION: GENE ENCODING LABYRINTHIN, A MARKER FOR CANCER
TITLE OF INVENTION: GENE ENCODING LABYRINTHIN, A MARKER FOR CANCER
TITLE OF INVENTION: GENE ENCODING LABYRINTHIN, A MARKER FOR CANCER
CURRENT PELLOTION NUMBER: US/09/659,521
CURRENT FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-17
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
LENGTH: 2442
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                                                                                                                                                                                                                                                                                                                        Length 2442
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Pred. No. 1.6e-224;
0; Mismatches 10;
Sequence 1, Application US/09659521
Patent No. 6727080
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                         Query Match 35.2%;
Best Local Similarity 98.8%;
Matches 825; Conservative
                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (70)..(834)
US-09-659-521-1
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TTCTTATGGCGACTGATGTAGATGATAGATTTGAGACCCTGGAACCTGAAGTATCTCAT TTTCTTATGGCGACTGATGTAGATGATAGATTTGAGACCCTGGAACCTGAAGTATCTCAT TTTCTTATGGCGACTGATGTAGCAGTGGAAGAGACCTGGAAGTATCTCAT GAAGAAACCGGGAAGAGACGGGAAGAGACAGTTTCACAAGAC GAAGGTAGAACCGGGAAGAGACGGGGAAGACGGAGAGACTTTTAATTTAATT TGTAATCAGGATATGGAAGAGATGATGTCTGAGCAGAAGACACGTGAAATTCAGTGAACCA	291 TGTAATCAGGATATGGAAGAGTGATGT	Patent No. 6812393 Patent No. 6812393 Patent No. 6812393
OY 781 ACCAAGTCTATGAGGAACAGGAGTATATGAACCTCTAGAAAATGAAGGATAGAAATCA 840 Db 665 ACCAAGTCTATGAGGAACAGGATTATGAACCTCTAGAAAATGAAGGGATAGAATCA 724 OY 841 CAGAAGTAACTGCTCCCTGAGGATAATGACGGTAATTGACAAGTAATTGAGAAG 900 Db 725 CAGAAGTAACTGTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGAGAAG 784 OY 901 AAGTAAGGATTTTTCCTGTGGAAGAACAGAAGATTCCACAGGTAATTGAGAAG 784 OY AAGTAAGCATTTTTCCTGTGGAAGAACAGAGAACACAACAACAACAACAAACA	RESULT 11 US-09-949-016-3447/C Sequence 3147, Application US/09949016 Fatent No. 681239 GENERAL INFORMATION: FALLICAT'S USTREEM OF TIVENTION: FALLICAT'S USTREEM OF TIVENTION: FILLE OF INVENTION: FILLE OF	Query Match 23.2%; Score 539.8; DB 4; Length 956;

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1490 carcactgraatraccratcrargcaagragrraaagagaragaagaartrggragrrrr 1431
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                                                   268 AGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATGAAAT 209
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tive 238; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                       485 GGTACACGCAGAACATGTTGAGGGAGAAGACTTGC 519
                                                                                                                                           208 GGTACACGCAGAACATGGTATGAATTAAAATCTGC 174
                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILING DATE:
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: AS-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT. Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELEPHONE: (703) 836-9300
TELEPHONE: (703) 831-4109
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                                                                                                                                                                                                                                                                      Sequence 14, Application US/08232463
Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.3%; So
Query Match
Best Local Similarity 7.2%; Pre
Matches 31; Conservative 238;
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 7218 base pairs
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STRANDEDNESS: single
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US-08-232-463-14/c
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US-09-949-016-122372/c

j Sequence 122372, Application US/09949016

j Sequence 122372, Application US/09949016

j Patent No. 6812339

j GENERAL INFORMATION

j TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION OF 0.04-14

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FEBLESCE FOR Windows Version 4.0
                                                                                                                                                                      RESULT 13

US-09-949-016-16453/C

JUNEAU 100-09-949-016-16453, Application US/09949016

Retent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOL1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFURANCE: FESTSEQ for Windows Version 4.0

LENGTH: 5746
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                                                                                 67054 TGGTTTGATCTTGTTGACTATGAGGAAGTTCTAGGTAA 67017
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89.5%; Pred. No. 4.7e-12;
ive 0; Mismatches 10
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Best Local Similarity
Matches 85; Conserv
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Matches 90; Conserv
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; ORGANISM: Human
US-09-949-016-122372
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; ORGANISM: Human
US-09-949-016-16453
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ò	939	939 CCACCAGAAACAAATAGAAAAACAGATGATCCAGAACAAAAAGCAAAAGTTAAGAAAAAG 998	866
qq	1310	1310 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	1251
ò	666	999 AAGCCTAAACTTTTAAATAAATTTGATAAGACTATTAAAGCTGAACTTGATGCTGCAGAA 1058	1058
QQ	1250		191
ò	1059	1059 AAACTCCGTAAAAGGGGAAAATTGAGGAAGCAGTGAATGCATTTAAAGAACTAGTACGC 1118	1118
Ор	1190		1131
ò	1119	1119 AAATACCCTCAGAGTCCACGAGCAAGATATGGGAAGGCGCAGTGTGAGGATGATTTGGCT 1178	1178
Ор	1130		1071
ò	1179	1179 GAGAAGAGA 1188	
qq	1070	1070 RRRRATCGCA 1061	
Searc Job t	Search completed: Ma Job time : 412 secs	Search completed: March 25, 2005, 14:35:49 Job time : 412 secs	

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190 8.2 158404 9 172 7.4 855 9 155 6.7 186676	130 5.6 126392 9 130 5.6 142265 9	26 103 4.4 941 9 AF224469 27 103 4.4 1254 9 AF184241 28 62 2.7 7339 4 BOVASBHY 29 60 2.6 60 6 COST414315	59 2.5 2208 6 59 2.5 2208 9 56 2.4 177614 2	40 1.7 556 4 35 1.5 4419 1 35 1.5 6024 1	35 1.5 6629 1 35 1.5 168569 1	39 32 1.4 524 1 40 32 1.4 1763 1	32 1.4 1951 1 32 1.4 2617 1	32 1.4 2770 1 32 1.4 2789 1 32 1.4 198991 1	46 31 1.3 566 1 47 31 1.3 919 1	31 1.3 988 1 31 1.3 1013 1	31 1.3 1733 1	52 31 1.3 2637 1 53 30 1.3 158289 2	29 1.2 234548 2 29 1.2 275547 2	56 27 1.2 27 6 57 27 1.2 2013 10	27 1.2 252366 2 26 1.1 6629 10	60 26 1.1 12095 10 61 24 1.0 1519 10	24 1.0 1680 10 24 1.0 2204 10	65 24 1.0 2221 10 65 24 1.0 110000 2 67 24 1.0 110000 2 67 24 1.0 110000 2	24 1.0 110000 8 24 1.0 150010 5	70 24 1.0 192578 5 71 24 1.0 222930 2	24 1.0 224556 10 24 1.0 289405 2	23 1.0 23 6 23 1.0 595 11	76 23 1.0 2483 10	23 1.0 3198 10	80 23 1.0 115135 10	23 1.0 120440 5 23 1.0 163122 2	23 1.0 192136 10 23 1.0 207761 3	85 23 1.0 210493 2 86 23 1.0 218311 2	87 23 1.0 220755 10 88 23 1.0 228016 2	23 1.0 239875 2 23 1.0 272016 3 23 1 0 273077 3	92 22 0.9 855 6
5.1.6 Compugen Ltd.		Search time 9715 Seconds (without alignments) 11591.346 Million cell updates/sec	cttgggaaactctggagaga 2324		residues		ers: 9416466											cted by chance to have a of the result being printed, score distribution.			-H)	AX146795 Sequence S83325 aspartyl(as	CQ871564 Sequence U03109 Human aspar	CQ729666 Sequence AF289489 Homo sani	AF306765 Homo sapi	HD234/6Z Gene enco AR274038 Sequence	AR44174 Sequence	AK53Z049 Sequence AX369081 Sequence	BC015518 Homo sapi BC025236 Homo sapi	CONTRACTOR SEQUENCE CONTRACTOR CO	AC021323 Homo sapi
GenCore version S Copyright (c) 1993 - 2005	OM nucleic - nucleic search, using sw model	Run on: March 25, 2005, 14:35:53 ; Sea (wi	Title: US-09-436-184-3 Perfect score: 2324 Sequence: 1 cggaccgtgcaatggcccag	Scoring table: OLIGO NUC Gapop_60.0 , Gapext 60.0	3 segs, 24227607955	Word size : 0	Total number of hits satisfying chosen parameter	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Listing first 100 summaries	Database : GenEmbl:*	2: gullan:	3: gD _ ln: * 4: gD _ on: * 5: gD _ on: *	6: 9D-04:* 7: 6h-ph-tr	8: 95 pm:	10: 9D_IO:* 10: 9D_IO:* 11: GD_RIE:*		14: gb_vi:*	Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score di	SUMMARIES	Query	SCOIE Macch Length UB	2324 100.0 2324 6 2324 100.0 2324 9 2222 96 6 2452 6	1766 76.0 2449 9	1164 50.1 1970 6 895 38.5 2680 9	684 29.4 2280 9 640 27 5 2442 6	9 640 27.5 2442 6 0 640 27.5 2442 6	1 640 27.5 2442 6 2 640 27 5 2442 6	3 640 27.5 2442 6	5 450 19.4 2761 9	9 89	9 190 8.2 132868 2

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COMMENT Authors note differences between this sequence and that of F. Korloth, C. Gieffers, and J. Frey: Gene 150 (2), 395-399 (1994), GenBank U03109. FEATURES Location/Qualifiers 1. 2324 /db_xref="taxon:9606" Coganism="Homo sapiens" Monit type="mRNA" Monit type="mRNA" J. 2324 J. 2324 Gene="aspartyl(asparaginyl)beta-hydroxylase, HAAH" CDS Gene="aspartyl(asparaginyl)beta-hydroxylase, HAAH"	w assentanonings se	Query Match 100.0%; Score 2324; DB 9; Length 2324; Best Local Similarity 100.0%; Pred. No. 0; 0; Mismatches 0; Indels 0; Gaps 0; Adtches 2324; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 0; Mismatches 0; Indels 0; Gaps 0; QV 1 CGGACCGTGCAATGGCCAAGAGACAGCAGCAGCAACAGCAGCAGCAGCGGGGGG	181 GGTTTATGGTGATTGCTGGGCGTCTGGACATCTGTAGCTTTGATC 240 181
Db 1561 CCGGAGATCCTGGCACTGATGATGAGAGATTTTATTTCCACCTGGGGGATGCCATGCAGA 1620	1801 1801 1861 1961 1921 1921 1981 1981 2041		Se3325 Se3325 LOCUS Se33325 LOCUS ACCESSION ACCESSION Se3325 LOCUS Se3326 LOCUS Se3

	1081 TTGAGGAAGCAGTGAATGCATTTAAAGAACTAGTAGGCAAATACCCTCAGAGTCCACGAG 1140 	1141 CAAGATATGGGAAGGCGCAGTGTGAGATTGGCTGAGAAGAGGAGAAGTAATGAGG 1200 	1201 TGCTACGTGGAGCCATCGAGACCTACCAGAGGTGGCCAGCCTACCTGATGTCCCTGCAG 1260	1261 ACCTGCTGAAGCTGAGTTTGAAGCGTCGCTCAGACAGGCAACAATTTCTAGGTCATATGA 132	1321 GAGGITCCCTGCTTACCCTGCAGAGATTAGTTCAACTATTTCCCAATGATACTTCCTTAA 1380	1381 AAAATGACCTTGGCGTGGGATACCTCTTGATAGGAGATAATGACAATGCAAAGAAAG	1441 ATGAAGAGGTGCTGAGTGTACCTAATGATGACGCTTTGCTAAAGTCCATTATGGCTTCA 1500 	1501 TCCTGAAGGCACAGAAATTGCTGAGAGCATCCCATATTTAAAGGAAGAATAGAAT 1560 	1561 CCGGAGATCTGGCACTGATGATGAGAGATTTTATTTCCACCTGGGGATGCCATGCAGA 1620	1621 GGGTTGGGAACAAAGAGGCATATAAGTGGTATGAGCTTGGGCAĞAAGAGAGACACTTTG 1680 	1681 CATCTGTCTGGCAACGCTCACACTGTGAATGGACTGAAAGCACAGCCTTGGTGGA 1740 	1741 CCCCAAAAGAAACGGGCTACACAGGGTTAGTAAAGTCTTTAGAAAGAA	1801 TCCGAGATGAAGGCCTTGCAGTGATGGATAAAGCCAAAGGTCTCTTCCTGCCTG	1861 AAAACCTGAGGGAAAAAGGGGACTGGAGCCAGTTCACGCTGTGGCAGCAAGGAAGAAGAA 1920 	1921 ATGAAAATGCCTGCAAAGGAGCTCCTAAAACCTGTACTACTAGAAAAGTTCCCCGAGA 1980 	1981 CAACAGGATGCAGAAGAGACAAATATTCCATCATGCACCCCGGGACTCACGTG 2040	2041 GGCCGCACACAGGCCCACAAACTGCAGGCTCCGAATGCACCTGGGCTTGGTGATTCCCA 2100	2101 AGGAAGGCTGCAAGATTCGATGTGCCAACGAGACCAGGACCTGGGAGGAAGGCAAGGTGC 2160
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126 120 186 180 246 240

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ACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAAAATGAAGGGATAGAAATCA 906
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                       CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCAGCGGCAACAGCAGCAGCAGCA
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Korioth,F.
Submitted (03-NOV-1993) Korioth F., Fakultaet fuer Chemie-Biochemie
II, Universitaet Bielefeld, Universitaetsstrasse 25, Bielefeld,
33615, Germany
                                                                                                                             PRI 30-NOV-1995
                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1 (Dases I to 2249)]
Korioth, F., Gieffers, C. and Frey, J. Cloning and characterization of the human gene encoding aspartyl beta hydroxylase
Gene 150 (2), 395-399 (1994)
            TCATCTTTGATGACTCCTTTGAGCACGAGGTATGGCAGGATGCCTCATCTTTCCGGCTGA
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Human aspartyl beta-hydroxylase mRNA, complete cds
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78. .2351
/function="hydroxylation of
residues"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="As-5"
/cell_type="mg63"
/cell_type="osteosarcoma"
/clone_lib="MG63-ZAP"
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QY 1081 TTGAGGAAGCAGTGAATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAGTCCACGAG 1140 Db 1147 TTGAGGAAGCAGTGAATGCATTTAAAGAACTAGTACGCAAATACCTCAGGAGTCCACGAG 1206 QY 1141 CAAGATATGCGAAGGCGCAGTGTGAGGATAATTTGGCTGAGGAAGAGAAATAATGAGG 1206 Db 1207 CAAGATATGGGAAGGCGAGTGTGAGGATGATTTGGCTGAGAGAGA	Oy 1261 ACCTGCTGAAGCTGAAGCTTGAAGCGTCAAGCAACAATTTCTAGGTCATATGA 1320 Db	1447 AAAATGACCTTGGCGTGGGATACCTCTTGATAGGAGATAATGACAATGCAAAGAAAG	Oy 1501 TCCTGAAGGCACAGAACTGCTGAGAGCATCCCATATTAAAGGAAGG	Oy 1621 GGGTTGGGAACAAAGAGGCATATAAGTGGTATGAGCTTGGGCACAAGAGAGGACACTTG 1680	ACTGGAAGTTAA ACTGGAAGTTAA GCCTGAGGATG	1861 1924 1921	1984	

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Dinchuk, J.B., Henderson, N.L., Burn, T.C., Hollis, G.F. and Dinchuk, J.B., Henderson, N.L., Burn, T.C., Hollis, G.F. and Direct Submission
Submitted (26-JUL-2000) Applied Biotechnology, DuPont Pharmaceuticals, P.O. Box 80400, Wilmington, DE 19880-0400, Updarmaceuticals, P.O. Box 80400, Wilmington, DE 19880-0400, Updarmaceuticals, Decation/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="8"
/map="8qt2 at STS WT-11767"
/tissue_type="liver"
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Homo sapiens aspartyl beta-hydroxylase 2.8 kb transcript mRNA, complete cds, alternatively spliced.
AF289489.1 GI:11878115
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1 (bases 1 to 2680)
1 inchuk, J.E., Henderson, N.L., Burn, T.C., Huber, R., Ho, S.P.,
Link, J., O'Neil, K.T., Focht, R.J., Scully, M.S., Hollis, J.M.,
Asparcyl beta - hydroxylase (Asph) and an evolutionarily conserved isoform of Asph missing the catalytic domain share exons with
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1 (bases 1 to 2442)
Radosevich, J.A.
Radosevich, J.A.
Gene encoding cancer marker labyrinthine
Patent: JP 2002512005-A 1 23-APR-2002;
JAMES A RADOSEVICH
                                                                                                        AGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAGATTTTGATGTGGATGATGCCAA
                                                                                                                                                       323 AGTITTATTAGACTTAAAGAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGG
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                                                        Score 684; DB 9;
Pred. No. 0;
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/db_xxef="G1"11991237"
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1 (Dases 1 to 2280)
Treves; S. Feriotto, G., Moccagatta, L., Gambari, R. and Zorzato, F. Molecular cloning, expression, functional characterization, chromosomal localization, and gene structure of junctate, a novel integral calcium binding protein of sarco(endo)plasmic reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treves, S. Feriotto, G., Moccagatta, L., Gambari, R. and Zorzato, F. Direct Submission
Submitted (19-SEP-2000) Experimental and Anesthesia and Research, University of Basel, Hebelstrasse 22, Basel 4031, Switzerland
                         GAGAACCACAACAAGAGGATGATGAGTTTCTTATGGCGACTGATGTAGATGATATG
                                      AGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGA
                                                                                          CAGTITCACAAGACIGTAATCAGGATATGGAAGAGATGATGTCTGAGCAGGAAAATCCAG
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mol_type="maxn."
db_xref="taxn.:9606"
/chromosome="8"
/map="8q12.1"
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Homo sapiens (human)
JP 2002512005-A/1
23-APR-2005
11-APR-1999 JP 2000536866
17-MAR-1999 US 09/040485
JAMES A RADOSEVICH
C12R15/09, CO7XL14/47, CO7XL16/18, C12P21/08, C12Q1/02, C12Q1/68// JGene encoding cancer marker labyrinthine
Key Location/Qualifiers
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                                                                                                                                   1 Similarity 99.9%; Score 640; DE Similarity 99.9%; Pred. No. 0; 90; Conservative 0; Mismatches

    .2442
    /organism="Homo sapiens"
/mol_type="genomic DNA"
    /db_xref="taxon:9606"

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                                                                             Unclassified.

1 (bases 1 to 2442)
Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S., Warg, T., Bangur, C.S., Manion, J. and Fan, L. Compositions and methods for the therapy and diagnosis of lung
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AR274038 2442 bp DNA.
Sequence 1791 from patent US 6504010.
                                                                                                                                                     Patent: US 6504010-A 1791 07-JAN-2003;
Location/Qualifiers
1. -2442
/mol_type="genomic DNA"
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Pred. No. 0
                                     GI:29705923
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Best Local Similarity 99.9%;
Matches 690; Conservative 0
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PAT 20-FEB-2004
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                                                                                                 Unknown.
Unclassified.
1 (bases I to 2442)
1 (bases I to 242)
Carter, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,
Carter, D., Retter, M.W., Mannion, J. and Fan, L.
Compositions and methods for the therapy and diagnosis of lung
                                                                                                                                                                                                                                                                              222 GCTGTCGTTTGGTTTGATCTTGTTGACTATGAGGAAGTTTCTAGGAAAACTAGGAATCTAT
106 GCTGTCGTTTGGTTTGATCTTGTTGATCTATGAGGAAGTTCTAGGAAACTAGGAATCTAT
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                                        AR44174 2442 bp DNA
Sequence 1791 from patent US 6667154.
AR441744.1 GI:42667904
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Patent: US 6667154-A 1791 23-DEC-2003;
Location/Qualifiers
1. .2442
/organism="unknown"
/mol_type="genomic DNA"
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Pred. No. 0;
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Best Local Similarity 99.9%;
Matches 690; Conservative 0
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Unclassified.

Unclassified.

S. Wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R., Vedvick,T.S., Catter,D., Retter,M.W., Mannion,J., Pan,L. and Wang,A.
Compositions and methods for the therapy and diagnosis of lung cancer.

VAL Patent: US 6509448-A 1791 21-JAN-2003;
ES Location/Qualifiers

1. 2442

/organism="unknown"
/mol_type="genomic DNA"
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27.5%; Score 640; DB 6; Length 2442;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 690; Conservative 0; Mismacches 1; Indels (
                    AR277619 2442 bp DNA
Sequence 1791 from patent US 6509448.
AR277619.1 GI:29711268
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CORIXA CORPORATION (US)
Location/Qualifiers
706 AATGAAGGGATAGAAATCACAGAAGTAACTG 736
                                                                                                                      AX369081 2442 bp Dr
Seguence 1791 from Patent W00204514.
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.5%; Score 640; DB 99.9%; Pred. No. 0; cive 0; Mismatches
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Sequence 1 from patent US 6727080.
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                         AATGAAGGGATAGAAATCACAGAAGTAACTG
    AR532049.1 GI:53920638
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source 11080 /organism="Homo sapiens" /mol type="mRNA" /db_xref="taxon:9606" /clone="lwAGE:3887962" /tissue_type="Lung, carcinoma, large cell undifferentiated." /clone llb="NIH MGC 69" /lab host="DH10B" /note="Wector: pCMV-SPORT6" 131080 /gene="AASPH" /note="AASPH" /note="AASPH" /db xref="LocusID:444"	/db_xref="MIM:60582" CDS 18905080 /gene="ASPH" /codon start=1 /producl="ASPH protein" /protein id="AAH15518.1" /db_xref="AG1:4418905" /db_xref="MIM:600581" /db_xref="MIM:600581"	REGGLSGTSFTWPWINGLANGE TO THE TRANSPORT OF THE TRANSPORT	Oy 1 CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCAGCAGCAGCAGCAGCAGCG 60	Oy 121 AGCATGGAGGACACAAGAATGGGAGGACACTCCGGGAACTTCATTCTTCACGT 180	Db TIGTTGATGAGGAAGTTCTAGGAATCTTGATGATGATGATGGATG	QY 481 AAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAACATGGACCCACAG 540
OY 762 GATACAGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAA 821	ACCESSION INAGES: 1887962), partial cds. ACCESSION BC015518.2 GI:34189304 VERSION BC015518.2 GI:34189304 SCHENDS Home sapiens (human) ORGANISM Home sapiens (human) ORGANISM Home sapiens (human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Home. AMTHORS STransherm R. I. Feinnel R. Gronse I. H. Derre I. C. B. ANTHORS STREEPENDE	Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Butcow, K.H., Schaefer, C.F., Batt, N.K., Hopkins, R.F., Jordan, H., Moorer, T., MaxS. I., Wang, J., Hsich, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleron, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., McKernan, K.J., Malek, J.W., Gunaratne, P.H., Richards, S., Morley, K.C., Malek, J.W., Garcia, A.M., Gay, L.J., Hulyk, S.W., W. Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., W. Worley, C., Maley, M., Gay, L.J., Hulyk, S.W., R., M., Mann, M., M., M., Mann, M., M., Mann, M., M., M., Mann, M., M., M., M., M., M., M., M., M., M.	Villalul, D., Muzlu, D.R., Sodergyen, L., Lu, J., Godrigues, S., Fabley, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Buckfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Gimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA semences	JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002). MEDLINE 22388257 REPERENCE 12477932 AUTHORS Strausberg,R. TITLE Direct Submission JOURNAL Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	REMARK NIH-MCC Project URL: http://mgc.nci.nih.gov On Aug 25, 2003 this sequence version replaced gi:15930166. Contact: MGC help dead of the properties of t	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LinL at: http://image.llnl.gov Series: IRAK Plate: 22 Row: d Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14589859. FEATURES Location/Qualifiers

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RKGGLSGTSFTWFNVIALLGVWTSVAVVWFDLVDYBEVLGKLGIYDADGDGDFDVDD
AKVLLGLKERSTSBPAVPPEBAEPHTBPEEQVPVBABPQNIEDEAKEQIQSLLHEMVH
AEHETEHSYHVEETVSQDCNQDMEEMMSEQENPDSSEPVVBDBRLHHDTDDVTYQVYB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MAQRKNAKSSGNSSSSGSGSGSTSAGSSSPGARRETKHGGHKNG"
through the I.W.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 42 Row: n Column: 19
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 14589865
This clone has the following problem: The cds is short compared to
the longest cds in the locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTCCGGCAGCGGTAGCACGAGTGCGGGCAGCAGCAGCCCCGGGGCCCCGGAGAGACAA 120
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                                                                                                                                                                                                                                                                    1. .2761

/organism="Homo sapiens"

/mol_type="mRNA"

/db xref="taxon:9606"

/clone="IMAGE:5090911"

/tissue type="Pancreas, epithelioid carcinoma"

/clone_lib="NHF MGC_42"

/lab host="Nector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="synonyms: JCTN, HAAH, CASQ2BP1, BAH"
/db xref="LocusID:44"
/db xref="MIM:600582"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.4%; Score 450; DB 9; L
99.8%; Pred. No. 1.3e-235;
iive 0; Mismatches 1;
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/product="ASPH protein"
/protein_id="AAH25236.1"
/db_xref="GI:19263911"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="LocusID:444"
/db_xref="MIM:600582"
                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 AAATGGTACACGCAGAACATG 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ASPH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 99.8 es 500; Conservative
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1. (bases 1 to 2761)

Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausher, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.R., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Mooret, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Maruslana, K., Earmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Banaldo, M.F., Casavant, T.L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Staplecon, M., Soares, M.B., Bosk, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunarane, P.H., Richards, S.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marza, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ברעשבע 2761 bp mRNA linear PRI 16-SEP-2003
Homo sapiens aspartate beta-hydroxylase, mRNA (cDNA clone
IMAGE:5090911), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Brin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Danne Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                              099
                                                                                                                                                                  778 AGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGA 837
                  718 GAGAACCACAACAAGAGGATGATGAGTTTCTTATGGCGACTGATGTAGATGATAGATTTG 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (05-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                              AGACCCTGGAACTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCCACGTGGAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   numan and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC025236
BC025236.1 GI:19263910
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Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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ORGANISM
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VERSION
KEYWORDS
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REFERENCE
AUTHORS
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AUTHORS
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JOURNAL
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MEDLINE
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Gaps

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1; Indels

9; Length 2761;

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180 366 240 426

300 486 360 546 420

909

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Namalia; Butheria; Primates; Catarrhini; Hominidae; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

B. 1 (bases 1 to 1608)

S. trausberg; R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Warg, J., Hsieh, F.,

Diatchenko, L., Maruslina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.B. Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Scheetz, T.B. Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Aramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.,

Villalon, D.K., Muzzy, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Butterfield, X.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Butterfield, X.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC066929 1608 bp mRNA linear PRI 02-MAR-2004
Homo sapiens cDNA clone MGC:87227 IMAGE:5264813, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 GACTTAAAGAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGGTGAGGCAAAA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                              453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CTGAGCCCGAGGAGGTTCCTGTGGAGCAGAACCCCAGAATATCGAAGATGAAGCAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 ACTTGCAACAAGAAGATGGACCCACAGGAGAACCACAACAAGAGGATGATGTTCTTA 240
  Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           514 ACTIGCAACAAGAAGAIGGACCCACAGGAGAACCACAACAAGAGGAIGAIGAIGAGTITCIIA 573
                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GACTTAAAGAGAGAGATCTACTACTTCAGAGCCAGCAGTCCCCGCCAGAAGAGGGCTGAGCCACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                              394 CTGAGCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACCCCCAGAATATCGAAGATGAAGCAA
                                                                                                                                                                                                                                                                                                                Gaps
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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0
                                                                                                                                                                                                                                                                   Length 297;
                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                              Query Match 12.8%; Score 297; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 2.7e-151;
Matches 297; Conservative 0; Mismatches 0;
                                                            PRECENTION ON 02068579-A 17305 06-SEP-2002;
PR Corporation (NY) (US)
Location/Qualifiers
1. .297
/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC066929.1 GI:44890460
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2 (bases 1 to 1608)
Strausberg, R.
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DEFINITION
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REFERENCE
AUTHORS
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                                                                                                              FEATURES
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                                                                                                                                     PAT 03-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GCCAGAAGAGGCTGAGCCCACACTGAGCCCGAGGAACAGGTTCCTGTGGAGGCAGAGCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATGAAATGGTACA 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 CCAGAATATCGAAGAAGAAGAAAGAAAGAAATTCAGTCCCTTCTCTCCATGAAATGGTACA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 GATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATCTTGTTGACTA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 TGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAGATTTTGATGT 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCAGAAGAGGCTGAGCCACACACTGAGCCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACC 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCACAGGAGAACCCACA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 25661 12-SBP-2002;
Chondrogene Inc. (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 315; DB 6; Length 366;
Pred. No. 3.2e-161;
0; Mismatches 1; Indels
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                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 bp DNA Sequence 17305 from Patent WO02068579. CQ731371. GI:42307776
                                                                                                                                     366 bp DNA Sequence 25661 from Patent WO02070737.

    .366
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

                                                                                                                                                                                                                                                                                                                                                                                                                            ne Inc. (CA)
Location/Qualifiers
AAATGGTACACGCAGAACATG 687
                                                                                                                                                                             CQ680735
CQ680735.1 GI:42196629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.7%;
Matches 365; Conservative
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Homo sapiens
                                                                                                                                                                                                                                            Homo sapiens (human)
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CQ731371
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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AUTHORS
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CQ680735
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Chases to 132868)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Petzhida, W., Forrest, C., Gage, D., Galagan, J., Ferreira, P., Fitzhida, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Howland, J.C., Liu, G., Looke, K., Macdonald, P., Marquis, N., McBwan, P., McGurk, A., McKernan, K., Morman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Sercianovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J. Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Direct Submission

All repeats sequence version replaced giil2229503.

All repeats we recommended to the seath Masker:
                                                                                                                                                                                                                                                                                                                                                    ACU21323 132868 bp DNA linear HTG 13-MAY-2001
Homo sapiens clone RP11-23M4, WORKING DRAFT SEQUENCE, 2 ordered
pieces.
                                                                      335 GGTTTATIGGTGATTGCATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGGCTTTGGTTTGATC 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ...-.-- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center clone name: 23 M 4

Center clone name: 23 M 4

Sequencing vector: M13; M77815; 3% of reads
Sequencing vector: Plasmid; n/a; 97% of reads
Sequencing vector: Plasmid; n/a; 97% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.96071

Consensus quality: 132571 bases at least Q40

Consensus quality: 132753 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washingcon.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: WIBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert size: 127000; agarose-fp
Insert size: 132768; sum-of-contigs
Quality coverage: 20.3 in Q20 bases; agarose-fp
Quality coverage: 19.5 in Q20 ba.
* NOTE: This is a 'working draft' sequence. It curre
* consists of 2 contigs. Gaps between the contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC021323.5 GI:14030007
HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens (human)
                                                                                                                                                          264
                                                                                                                                                                                                                   395 rigirgaciardaggaagriciag 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birren, B., Linton, L., Nusbaum, Homo sapiens, clone RP11-23M4
                                                                                                                                                          241 TTGTTGACTATGAGGAAGTTCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 132868)
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                                181
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KEYWORDS
SOURCE
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AC021323
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AUTHORS
TITLE
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                                                                                                                                             UNH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein (NHGRI) & Shiraki
Tissue Procurement: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Pieror Carninci (RIKEN)
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Contact: Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Incre"Asp-B-Hydro N; Region: Aspartyl beta-hydroxylase N-terminal region. This family includes the N-terminal regions of the junctin, junctate and aspartyl beta-hydroxylase proteins. Junctate is an integral BR/SR membrane calcium binding protein, which comes from an alternatively spliced form of the same gene that generates aspartyl beta-hydroxylase and junctin. Aspartyl beta-hydroxylase the post-translational hydroxylation of aspartic acid or asparagine residues contained within epidermal growth factor (BGF) domains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 167 Row: k Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14589865. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/podoc="Unknown (protein for MGC:87227)"
/prodecin_id="AAN66929_1"
/db_xref="G1:44890461"
/db_xref="G1:44890461"
/kranslation="MAQRKNAKSSGNSSSSGSGSSTSAGSSSPGARRETKHGGHKNG RKGGLSGTSFFTWRYTALLGYWTSVAVVWFDLVDYEEVLAKKDFRYNLSEVLOGKLGIYDADGGGDFPDVDDAKVLALGITKDGSNENIDSLEEVLNILAEESSDWFYGFLSFLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGCAGCAGCAGCAACAAGCAGCAGCG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AGCATGGAGGACACAAGAATGGGAGGAAAGGCGGACTCTCGGGAACTTCATTCTTCACGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 AGCATGGAGGACACAAGAATGGGAAGGAAAAGGGGGACTCTCAGGAACTTCATTCTTCACGT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                         Submitted (01-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTPFEMLEEEEESETADGVDGTSQNEGVQGKTCVILDLHNQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue type="Brain, hippocampus"
clone_lib="NIH_MGC_95"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.2%; Score 213; DB 9; L
99.6%; Pred. No. 5.5e-105;
tive 0; Mismatches 1;
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Marquis, N. Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Murphy, T., Maylor, J., Magues, L., Maldin, J., Menes, L., Malora, T., Schupback, R., Seaman, S., Severy, P., Sutacos, M., Scharo, S., Schupback, R., Seaman, S., Severy, P., Straues, M., Sharos, T., Talams, J., Tesfaye, S., Theodora, J., Travers, M., Sharos, T., Trigillo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Zimmer, A. and Zody, M. J., Young, G., Zainoun, J., Direct Submission of Trigillo, J., Vassillev, H., Viel, R., Vo, A., Milson, B., Linton, D., Milson, B., Malora, S., Erraus, M., Trigillo, J., Vassillev, H., Viel, R., Vo, A., Malora, D., Malora, M., Sachan, D., Ye, M. J., Young, G., Zainoun, J., Direct Submission of Travers, M., Masten, V., Ye, M. J., Young, G., Zainoun, J., Direct Submission of Travers, M., Masten, D., Ye, M. J., Young, G., Zainoun, J., Malora, J., Malora, J., Malora, M., Basten, V., Bloom, T., Boukhgalter, B., Barra, M., Basten, V., Bloom, T., Boukhgalter, B., Linton, L., Musbaum, C., Lander, E., A., Malora, J., S., Dedge, S., Gards, S., Barra, M., Basten, V., Delwar, K., Diara, J. S., Dodge, S., Gards, S., Gords, S., Goyete, M., Gago, M., Gago, M., Gago, M., Colmago, M., Collins, S., Collymore, M., Marters, A., Kells, C., Larger, M., Marters, A., Kells, C., Larger, M., Marchis, A., Kells, C., Larger, M., Marchis, A., Kells, C., Macdonald, P., Marchis, M., Marchis, M., McBana, M., Kells, C., Macdonald, P., Marchis, M., Malora, M., McBana, M., Kells, C., Macdonald, P., Marchis, M., Marchis, M., McBana, M., Kells, M., Marchis, M., McBana, M., Marchis, 
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/mol_type="genomic DNA"

/db_xref="texon:9606"

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complement (1697. .1825"
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Center clone name: 252_C_19
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Homo sapiens chromosome 8, clone RP11-252C19, complete sequence.
AC090094
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2 (bases 1 to 158404)
3 (barren, B. Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barren, B., Linton, L., Boguslavkiy, L., Boukhgalter, E., Brown, A., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farchira, P., Fitzhugh, W., Gage, D., Galagan, J., Bodge, S., Farchira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Govette, M., Graham, L., Grand-Plerre, N., Hagos, E., Heaford, A., Horton, L., Hulme, W., Iliev, T., Johnson, R., Jones, C., Karatas, A., Lancque, K., Lamazares, R., Landers, T., Lahccx, Lamazares, R., Landers, T., Lahckey, L., Landers, T., Landers, Landers, Landers, T., La
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1 (bases 1 to 158404)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone RP11-252C19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 130483; contig of 13083 bp in length 130384 132868; contig of 2385 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="RPCI-11 Human Male BAC"
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2195 GCAGGATGCCTCATCTTTCCGGCTGATATTCATCGTGGATGTGTGGCATCCGGAACTGAC 2254
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I (bases 1 to 85)

Lim, K.Y.; Hong.C.S. and Kim, D.H.

CDNA cloning and characterization of human cardiac junctin 20432113

10974562

2 (bases 1 to 855)

Lim, K.Y.; Hong.C.-S. and Kim, D.H.

Direct Submission
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8.2%; Score 190; DB 9; Length 158404;

Best Local Similarity 100.0%; Pred. No. 2.7e-92;

Matches 190; Conservative 0; Mismatches 0; Indels 0;
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complement(3874. 39178)
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complement(39345. 39549)
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Young, G., Zainoun, J., Zimmer, A. and Zody, M. TITLE Direct Submission Submitted (27-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA REPERBNCE 3 (bases 1 to 186676) BITEN, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barnah, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cook, P., Parelian, P., FitzHugh, W., Cage, D., Galagan, J., Gardyna, S., Faro, S., Fareira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Johnson, R., Landers, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marguis, N., Matthews, C., MacLean, C., Norman, P., McRennan, K., McBheeters, R., Melleim, J., Mengue, L., Norman, C., Conner, T., Obnson, C., Norman, C., Norman, C., Norman, C., McGarby, C., Danger, C., Norman, C., McGarby, C., Landers, C., Norman, C., McGarby, C., Conner, C., Conne	Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Reta, R., Rieback, M., Rilae, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Schauer, S., Schauer, S., Schupback, R., Seman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triglilo, J., Vassilitev, H., Viel, R., Voh., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. TITLE Direct Submission JOURNAL Submission JOURNAL Glasserotte, Cambridge, MA 02141, USA COMMENT On Sep 28, 2001 this sequence version replaced gl:15422051. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html Center: Whitehead Institute/ MIT Center for Genome Research Center: Code: WIBR Web site: http://www.seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu Center project name: 18165	PEATURES
JOURNAL Submitted (13-JAN-2000) Life Science, Kwangju Institute of Science and Technology, Kwangju 500-712, Korea Location/Qualifiers 1. 485 Location/Qualifiers 1. 485 Location/Qualifiers 1. 485 Location/Qualifiers 1. 585 Location/Qualifiers 1. 74 Location/Qualifiers 1. 85	Query Match 7.4%; Score 172; DB 9; Length 855; Best Local Similarity 100.0%; Pred. No. 2.2e-82; Ace 82; Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0; O; Indels 0; Gaps 0; Qy 162 GGAACTTCATTCACGTGGTTATGCATTGCTGGGCGTCTGGACATTGTTGGACATTGTTGGACATTGTTGGACATTGTTGGACATTGTTGGATTGTTTGT	H. H

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Compositions and methods relating to osteoarthritis
Patent: WO 02070737A 2707 12-SEP-2002;
Chondrogene Inc. (CA)
Location/Qualifiers
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100.0%; Pred. No. 5.3e-62;
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Best Local Similarity 100.0%; Pred. No. 5.4e-73;
Matches 155; Conservative 0; Mismatches 0;
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    .191
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Esten, B., Linton, L., Bouchalla, C., Lander, E., Allen, N., Anderson, S., Barren, M., Bastien, V., Boqualavkiy, L., Boukhgalter, B. Brown, A. Camarata, J., Campopiano, A., Chong, J., Choepel, Y., Colangelo, M., Callymore, A., Cocke, P., Dearellano, K., Dewar, K., Diaz, J., S., Dodge, S., Farcs, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Galoe, S., Govette, M., Caham, L., Gardyna, S., Ginde, S., Govette, M., Carbam, L., Gardyna, S., Ginde, S., Govette, M., LaRocque, K., Indees, T., Hagos, B., Haeford, A., Horton, L., Hullme, W., Iliev, I., Johnson, R., McRenan, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Mencus, L., McCarthy, T., Obonnell, P., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Mencus, L., Morman, C.H., O'Connor, T., Obonnell, P., O'Nell, D., Oliver, J., Peterson, K., Phukhang, P., Peterson, K., Phukhang, P., Peterson, K., Phukhang, P., Peterson, K., Phukhang, P., Sances, R., Schupback, R., Samon, S., Severy, P., Sougnez, C., Spencer, B., Stanger, S., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stanger, S., Schupback, R., Samon, C., Noran, C., Wolf, M., Strauss, M., Subramanian, N., Trigilla, T., Vassillev, H., Viel, R., Vol, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Sarion, B., Mu, X., Wyman, D., Ye, W. J., Young, G., Sarion, B., Mu, X., Wyman, D., Ye, W. J., Young, G., Sarion, B., Mu, X., Wyman, D., Ye, W. J., Wolfer, S., Gord, S., Carate, B., Mu, X., Wyman, D., Ye, W. J., Wolfer, S., Ferreira, P., Fitzer, B., Mu, X., Wyman, D., Ye, W. J., Wolfer, S., Ferreira, P., Fitzer, M., Moy, J., Matthews, C., Karaasa, A., Kalle, C., Lander, R., Majos, J., Sarion, J., Mulle, W., Illev, I., Johnson, R., Danes, I., Mayor, J., Matthews, C., Macchan, J., Mulle, W., Illev, I., Johnson, R., Wayan, C., Whung, S., Gord, S., Carate, S., Schupback, R., Saman, S., Theodore, J., Tropham, K., Travers, M., Yassillev, H., Wuller, W., Waller, M., Wayan, D., Y
                                                                                       ACU91173 142265 bp DNA linear PRI 16-OCT-2002
Homo sapiens chromosome 8, clone RP11-280G9, complete sequence.
AC091173
                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 14228)
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Birren, B., Nusbaum, C., Lander, B., Alli, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chararo, B., Chopel, Y., Collymore, A., Cook, A., Cooke, P., Dewrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gard, Ma., Gage, D., Galagan, J., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kelle, C., Landers, T., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J.,
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Homo sapiens chromosome 8, clone RP11-280G9
                                                                                                                                                                                                GI:24022446
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Birren, B., Linton, L.,
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Homo sapiens
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                                RESULT 25
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare cocasion of the clone being a XAC. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EmBi. Sw: SwiSSPROT: Tr: TREMBL; WP:, WORMPEP; Information the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/Celegans/wormpep XX-NCH21113M21 is from a Cancer cell lines BACS library VECTOR: pBACE3.6_BamHI.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 126392)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (27-JUL-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
487 TACACGCAGAACATG 501
                                    121 TACACGCAGAACATG 135
                                                                                                                                                                                                                                                                                                                                                                                  sapiens (human)
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CR626894/c
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Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Nochu, C., Nordan, C.H., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Reil, D., O'Isil, D., O'Isil, D., O'Reil, D., O'Reil, D., O'Reil, D., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Schupback, R., Stojanovic, N., Talamas, J., Roy, A., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theedore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Wo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

L. Submitted (16-OCT-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

ON Oct 16, 2002 this sequence version replaced gi:27758785.

All repeats were identified using RepeatMasker:
Smit, A.F. A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Center project Information
Center project name: L12773
Center clone name: 280_G_9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="RP11-280G9"
clone_lib="RPCI-11 Human Male BAC"
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4833. .4956
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complement (5342. .5468)
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rpt_family="MER103"
152. .6606
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734. .8035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="MLT2B1"
286. .1579
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664. .7686
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076. .8174
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537. .4750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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701. .1725
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740. .4529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rpt_family="L1MB5"
755. .4832
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137221 GATGAGTTTCTTATGGCGACTGATGTGATGATAGATTTGAGACCCTGGAACTGAAGTA 137280
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100.0%; Pred. No. 3.2e-59;
ative 0; Mismatches 0;
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                                                                                                                                                                                                             family="AluJb"
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omplement(14137, .14441)
rpt family="AluSq"
4853, .14864
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omplement(15394. .16172)
rpt family="HSMAR2"
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omplement(21202. .21411)
rpt family="MIR"
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                                                                                                                                                                                                                                                                                                               rpt family="AT rich"
omplement (14865. .153
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omplement(16203..16
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rpt_family="AT_rich"
9538. .19653
                                                                                                                                                                                  1649. .13675
rpt family="(TGAA)n"
omplement(13775. .14
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                                                                                       /rpt_family="MER5A"
1730. 1181
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omplement(20586. ..
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complement(22445...
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                                              rpt_family="MER5A"
1330. .11610
                                                                                   rpt_family="AluSg"
1620. .11729
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rpt_family="MIR" 0946. .11255
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pt_family="L2"
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                            family="L2"
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3151. .18250
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Bos taurus aspartyl (asparaginyl) beta hydroxylase mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (15-APR-1992) P.A. Friedman, Merck Sharp and Dohme
Research Laboratories, West Point, PA 19486 USA
Original source text: Bos taurus cDNA to mRNA.
Location/Qualifiers
2 (bases 1 to 1254)
Wetzel,GT., Ding.S. and Chen,F.
Wetzel,GT., Ding.S.
Bubitted (08-SEP-1999) Pediatrics Cardiology, UCLA School of Medicine, 675 Charles E. Young Drive South, Los Angeles, CA 10055-7045, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (Date 1 to 2739)
Jaja, S., Vanbueen, W.J., Diehl, R.E., Kohl, N.E., Dixon, R.A., Elliston, K.O., Stern, A.M., and Friedman, P.A.
cDNA cloning and expression of bovine aspartyl (asparaginyl)
bera-hydroxylase
J. Biol. Chem. 267 (20), 14322-14327 (1992)
                                                                                                                                      1. 1254

/ Organism="Homo sapiens"

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/ Ab Xref="taxon:9666"

/ tissue_type="heart"

42. 719

/ note="junctional sarcoplasmic reticulum protein;

/ codon_start=in binding protein"
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100.0%; Pred. No. 2.4e-44;
tive 0; Mismatches 0; Indels
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M91213.1 GI:162693
aspartyl (asparaginyl) beta hydroxylase.
Bos taurus (cow)
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2 (bases 1 to 2739)
Friedman, P.A.
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Best Local Similarity 100.0
Matches 103; Conservative
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GKKOREKEKVOLEKSAKTKENRKKSTNMKDVSSKMASRDDRKESRSSTRYAHLTKG
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Homo sapiens
Bukaryoea; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1254)
Makzel, CT., Ding,S. and Chen,F.
Molecular cioning of junctin from human and developing rabbit heart
20232172
10767180
                                                                                                                                                                                                                                                                                                                                                                        Lim.K.Y., Hong, C.-S. and Kim, D.H.
Lim.K.Y., Hong, C.-S. and Kim, D.H.
Lim.K.Y., Hong, C.-S. and Kim, D.H.
Direct Submission
Submitted (13-JAN-2000) Life Science, Kwangju Institute of Science
and Technology, Kwangju 500-712, Korea
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRI 18-MAY-2001
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1 (bases 1 to 941)

Lim, K.Y., Hong, C.S. and Kim, D.H.

cDNA, K.Y., oloning and characterization of human cardiac junctin

Gene 255 (1), 35-42 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/db_zref="taxon:9606"
/tissue type="heart"
87 764
/note="junctional sarcoplasmic reticulum protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ttch
31 Similarity 10.0%; Pred. No. 246-44;
103; Conservative 0; Mismatches 0; Indels
                                                                  941 bp mRNA linear
Homo sapiens junctin isoform 1 mRNA, complete cds.
AF224469
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Homo sapiens cardiac junctin mRNA, complete cds.
AF184241
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Gaps

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start=1
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ATPase; glycoprotein.
Homo sapiens (human)
Homo sapiens
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             Homo sapiens (human)
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                                Homo sapiens
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KTI KAELDAAEKLRKEGKI EEANNA FEELVRKYPOSPGARVKKKKFPLINKFD
KTI KAELDAAEKLRKEGKI EEANNA FEELVRKYPOSPGARVKRAGCEDLAEKRRSNE
ALKRADIGVOYLLI GONDSAKKYYEEVLSVTPROPOGPGARVKSLLILQKLVOLPPDDT
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LRMHLGLVI PKEGCKI RCANETRTWEEGKVLI FDDS FEHEVWQDAASFRLI FI VDVWH
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                                                                                   /translation="MAPRKNAKGGGGNSSSSSGSPTGCTSGGSSSPGARRETKQGGL
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                                                                                                                                           I EDEVYEQVQSLDETVYSEPGENLPQEPEGPAEELQPDDHVFVGSDADDRYEPWGTGA
VHEETEDSYHI EETASPAYSQDMEDMMYEQENPDSSEPVVVDDAERTYQETDDVTYRD
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S. Oligonuclectide library for detecting rna transcripts and splice variants that populate a transcriptome Patent: WO 0210449-A 11070 07-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GACTGTAATCAGGATATGGAGATGATGTCTGAGCAGGAAAATCCAGATTCCAGTGAA
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/protein_id="AAA03563.1"
/db_xref="GI:162694"
'translarion':
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1.2e-20;
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Sequence 322 from Patent WO03004646.
AX771609.1 GI:32438407
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llarity 100.0%; Pred. No. 1.2
Conservative 0; Mismatches
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/mol_type="unassigned DNA"
/db xref="taxon:9606"
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CQ541435.1 GI:41507699
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Matches 60; Conserv
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PRI 18-MAY-1995 ·
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/db_xref="GI:28933"
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/tb_xref="UniProt/Swiss-Prot:P05026"
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INIVRELEKYKOSAORDDMIFEDCGDVPSEPKERGDFNHERGERKVCRFKLEWLGNCS
GLNDETYGYKEGKPCIIIKLNRVLGFKPKPRKNESLETYPVMKYNPNVLPVQCTGKRD
EDKDKVGNVEYFGLGNSPGFPLQYYFYYGKLLQPKYLQPLAVQFTNLTMDTEIRIEC
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                            O'Mahony, D.J., Byrne, D., Brayden, D., Lambkin, I. and Higgins, L. Genetic analysis of Peyers's patches and M cells and methods and compositions targeting Peyer's patches and M cell receptors Patent: W0 3004646-A 322 16-JAN-2003; ELAN CORPORATION, Plc (IE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="unnamed protein product; put. Na/K-ATPase beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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Kawakami, K., Nojima, H., Ohta, T. and Nagano, K.
Molecular cloning and sequence analysis of human Na, K-ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Data kindly reviewed (10-AUG-1986) by K. Kawakami.
Location/Qualifiers
1. .2208
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                                                                                                                                                                                                                                                                                                                                                                                                                            2.5%; Score 59; DB 6; Le
100.0%; Pred. No. 4.3e-20;
tive 0; Mismatches 0;
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note="pot. glycosylation site"
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Human mRNA for Na/K-ATPase beta subunit.
X03747
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1485. .1490
note="pot. polyA signal"
2001. .2006
                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="unassigned DNA"
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2 [ Dages I to 177614)

Milosavijevic,A., Sodergran, E., Cauros, M., Li, B., Jackson, A.R., Adams, C., Adio-Oducla, B., Adi-Osman, F.R., Allen, C., Adisbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Bentcon, J., Bimage, K., Burmell, E., Brown, M., Bryant, N.P., Buhay, C., Bentcon, J., Elieva, M., Brown, B., Brown, M., Bryant, N.P., Buhay, C., Carron, F.F., Carter, M., Cavasos, S.R., Chacko, J., Chavez, D., Char, G., Chen, R., Chiu, D., Chowdhry, J., Christopoulos, C., Claveland, C.D., Cox, C., Coyle, M.D., Dathorne, S. R., David, R., David, M., Davis, C., Dann, R., Dann, A.L., Ding, Y., Dinh, H.H., Douthwate, R., David, R., David, M., Davis, C., Dann, A.L., Ding, Y., Dinh, H.H., Douthwate, R., David, M., Davis, C., Claveland, C.D., Cox, C., Coyle, M.D., Dathorne, S. R., David, R., David, R., David, M., Davis, C., Claveland, C.D., Cox, C., Coyle, M.D., Dathorne, S. R., David, R., David, R., David, M., Davis, C., Claveland, C.D., Dann, A.L., Ding, Y., Dinh, H.H., Douthwate, R., David, R., David, R., David, R., David, R., David, R., Garcia, A., Barling, C., Emerling, S., Baccito, M., Falls, T., Farraguo, D., Garcia, A., Harris, C., Harris, C., Harris, C., Harris, C., Harris, R., Harris, M., Haylak, P., Hawes, A., Holline, B., Homsi, F., Howard, S., Huber, J., Holline, B., Homsi, F., Howard, S., Huber, J., Holline, B., Homsi, F., Howard, S., Huber, J., Holline, B., Howsi, E., Lawis, L., Landry, M., Loulse, B., Loudh, S., Loudh, S., Karlly, S., Khan, U., X., Lucier, A., Lucier, R., Martindale, A., Matcher, M., Malle, M., Moren, M., Morris, S., Moser, M., Neu, Y., Maheshwari, M., Malle, M., Nokuon, G., Oragunye, N., Oragunye, N., Oragunye, N., Neu, E., Parker, S., Parker, S., Savery, G., Scherer, S., Scott, G., Scherer, S., Savery, G., Scherer, S., Tanerise, R., Ta
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1 (basea 1 to 177614)

Csuros, M. and Milosavljevic, A.

Pooled genomic indexing (PGI): mathematical analysis and experiment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA linear HTG 09-APR-2003
                                                                                                                                                                                                                                                                                                                        2239 GGCATCCGGAACTGACACCACAGCAGAGGCGCGCTTCCAGCAATTTAGCATGAATTC 2297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (in) Guigo, R. and Gusfield, D. (Eds.);
ALGORITHMS IN BIOINFORMATICS, SECOND INTERNATIONAL WORKSHOP, WABI
2002, ROME, ITALY, SEPTEMBER 17-21, 2002, PROCEEDINGS: 10-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                             59 GGCATCCGGAACTGACACCACACGCAGAGACGCAGCCTTCCAGCAATTTAGCATGAATTC 1
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Best Local Similarity 100.0%; Pred. No. 4.3e-20;
Matches 59; Conservative 0; Mismatches 0;
/note="pot. polya signal"
2026. .2031
/note="pot. polyA signal"
2187. .2193
/note="pot. polyA signal"
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Macaca mulatta clone CH250-267C14,
AC143562
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Macaca mulatta (rhesus monkey)
Macaca mulatta
                          misc_feature
                                                                                      misc_feature
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REFERENCE AUTHORS

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* NOTE: Estimated insert size may differ from sequence length

(See http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: The contigs are based on the application

* of the PGI method using the Human genome (NCBI build 31)

* as the comparative genome.

* NOTE: This is a 'working draft' sequence. It currently

* consists of I contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CFU38414 1777 bp mRNA linear MAM 02-FEB-1996 Canis familiaris junctional sarcoplasmic reticulum protein mRNA, complete cds.
                                                                                                                                                                                                                                                           Direct Submission
Submitted (09-APR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warten, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wheczyk, R., Woden, S., Worley, K., Wu, C., Wu, Y., Wu, S., Zhou, J., Zorvilla, S., Kucherlapati, R., Weinstock, G. and Gibbs, R., Uppublished
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Best Local Similarity 100.0%; Pred. No. 2e-18;
Matches 56; Conservative 0; Mismatches 0; Indels
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/note="assembly_name:CH250-267C14.1B
CONFIDENCE:_0.67"
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/mol_type="genomic DNA"
/db_xref="taxon:9544"
/clone="CH250-267C14"
                                                                                                                                                                                                        (bases 1 to 177614)
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Gaps

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AF289486
Mus musculus aspartyl beta-hydroxylase 4.5 kb transcript (Asph)
mRNA, complete cds; alternatively spliced.
                                                                                                                                                                                /translation="Liggwisyavvwpelvdyeevlgkigvydadgdgdfdvddakal
leepggvakrkykvkelikeelkkgkekpesrreskheerkrgkkekebsrkggki
aasdvsrrespagkkskekekaesaktkenrkkstptkdlsskwaprdtddrkesrss
nqlttlakgnshkrkw"
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Dinchuk, J. E., Henderson, N. L., Burn, T. C., Huber, R., Ho, S. P., Link, J., O'Neil, K. T., Focht, R. J., Scully, M. S., Hollis, J. M., Aspareyl beta -hydroxylase (Asph) and an evolutionarily conserved isoform of Asph missing the catalytic domain share exons with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (26-UUL-2000) Applied Biotechnology, DuPont Pharmaceuticals, P.O. Box 80400, Wilmington, DE 19880-0400, USA Location/Qualifiers
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Dinchuk,J.E., Henderson,N.L., Burn,T.C., Hollis,G.F. and
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alternatively spliced"
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                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 556;
1.2e-09;
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/tissue_type="liver"
                                                                                                                                                                                                                                                                                                                                                       1.7%; Score 40; DB 100.0%; Pred. No. 1.2 Live 0; Mismatches
                                                                                                     /product="cardiac junctin"
/protein_id="AAF37204.1"
/db_xref="GI:7141075"
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/mol_type="mRNA"
/strain="BALB/c"
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/chromosome="8"
'db xref="taxon:9986"
                         /tissue type="heart"
<1, .531
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                                                                             /codon_start=1
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/gene="Asph"
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Best Local Similarity
Matches 40; Conserv
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AF289486
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Oryctolagus cuniculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Chordata, Leporidae, Oryctolagus.

1 (bases 1 to 556)
Wetzal, Gr., Ding, S. and Chen, F.
Wolecular cloning of junctin from human and developing rabbit heart
Mol. Genet. Metab. 69 (3), 252-258 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryccolagus cuniculus cardiac junctin mRNA, partial cds.
AF198966
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2 (bases 1 to 556)
2 (bases 1 to 556)
Wetzel, G.T., Ding, S. and Chen, F.
Wetzel, G.T., Ding, S. and Chen, F.
Direct Submission (26-072-1999) Pediatrics Cardiology, UCLA School of Submitted (26-072-1999) Pediatrics Cardiology, UCLA School of Medicine, 675 Charles E. Young Drive South, 3754 MRL Building, Los Medicine, 675 Charles E. Young Drive South, 3754 MRL Building, Los Angeles, CA 90095-7045, USA
Angeles, CA 90095-7045, USA
Angeles, CA 90095-7045, USA
Angeles, CA 90095-7045, USA
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/db_xref="G1:10163913"
/db_xref="G1:10163913"
/db_xref="G1:1163913"
/db
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                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. 1 (Dases I to 1777) Jang, L., Sanborn, K., Jorgensen, A.O. and Kelley, J. Purification, primary structure, and immunological characterization of the 26-kpa caleguetrin binding protein (junctin) from cardiac
                                                                                                                                                                                                                                                                                                               CardionOpp. 111 W. 10 Street, Indianapolis, IN 46202, USA
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Llarity 100.0%; Pred. No. 8.6e-17;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /ti§sue_type="heart"
89. .721
Anction="calsequestrin binding protein"
/note="junctin"
                                                                                                                                                                                                       junctional sarcoplasmic reticulum
J. Biol. Chem. 270 (51), 30787-30796 (1995)
96107245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
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Matches 53; Conserv
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join (AF289205.1:1772. .2075, AF289206.1:1105. .1173, AF289207.2:4438 .4512, AF289207.2:14455 .4512, AF289207.2:14458 .4512, AF289207.2:1689207.2:16892 .1584, AF289207.2:16892 .15854, AF289207.2:16892 .15857, AF289207.2:16892 .15857, AF289207.2:16893 .15921, AF289207.2:16893 .15921, AF289207.2:16893 .15921, AF289207.2:16893 .15921, AF289207.2:16893 .15921, AF289208.1:1520 .1665, AF289200.1:292 .378, AF289208.1:1520 .1665, AF289200.1:292 .378, AF289211.1:1764 .2056, AF289210.1:4279 .4415, AF289211.1:1764 .2056, AF289210.1:4279 .4415, AF289211.1:1764 .2056, AF289214.1:5805 .5938, 1665 .>6000) AF289212.1:1286 .565, AF289214.1:5805 .2184, AF289206.1:105 .1173, AF289207.2:1428 .565, AF289207.2:1438 .4512, AF289206.1:105 .1173, AF289207.2:1428 .1004, AF289207.2:1428 .1004, AF289207.2:1428 .1004, AF289207.2:12897 .1825, AF289201.1:1280 .1865, AF289207.2:12897 .4415, AF289207.2:12897 .1825, AF289201.1:1280 .1865, AF289207.2:12897 .4415, AF289201.1:1280 .1865, AF289210.1:292 .378, AF289211.1:3860 .5451, AF289211.1:2999 .2023, AF289211.1:3860 .5451, AF289211.1:2999 .2023, AF289211.1:3860 .5451, AF289211.1:2999 .2023, AF289211.1:360 .5451, AF289211.1:2099 .2023, AF289211.1:360 .5451, AF289211.1:2099 .2023, AF289214.1:5805 .5893, 1665 .1815) AF289214.1:5805 .5938, 1665 .1815) AF289214.1:3860 .5451, AF289211.1:2099 .2023, AF289214.1:3860 .5451, AF289211.1:2099 .2023, AF289214.1:2000 .1805, AF289214.1:2000 .2000 .84515, AF289214.1:5805 .8938, 1665 .1815) AF289214.1:3860 .5938, AF289214.1:5805 .8938, AF289214.1:2000 .2000 .854114 .2000 .2000 .854114 .2000 .2000 .854114 .2000 .2000 .854114 .2000 .2000 .854114 .2000 .2000 .854114 .2000 .2000 .854114 .2000 .2000 .854114 .2000 .2000 .854114 .2000 .20
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Mus musculus aspartyl beta-hydroxylase 6.6 kb transcript (Asph)
mRNA, complete cds; alternatively spliced.
AF289487
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 6629)
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/gene="ASPH"
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/gene="ASPH"
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Matches 35; Conserva
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AF289487
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SILGESVHTDHDLEADGLAGEROPEVEDFLTTTDSDEAFESTEDLEDGTVEGUE
DYSOMHENDWEBWTNEQDRADESDEAFESTHAESVHQDYDEPVTSESEHEGY
BISDNTIDDSSILGESTIVARYSUESCOTTPRYKKKKKLLAKFDRTILKDHGAGVGTLLAG
BYGTESLAVARFEELVRKYPOSPRARYGRACCEDDLAEKGRSNEVLRALDAAEKLAR
PDAPTDLVKLSLKRSERGOTGHNRGSLLTLGGLAKCRNEVLRALIGGDVGTLLAG
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NDSAKKYTEEVLAVTPDOGFAKVHYGFLIKAGOKKSESTIVADGAGVGTLLAG
NDSAKKYTEEVLAVTPEDGARKHYGFLIKAGOKKSESTIVADGAGVGTLAGD
NTGARETRANKLIRDEGLAVMDKAKGLFLPEDENLAEKGDWSGFTLWQCRRANALGAGVT
IRCANETRTWEEGKVLIPDDSFEHEVWODASSFRLIFIVDVWHPELTPQQRRSLPAI"

1395. . 4419

/gene="Asph"
/gene="Asph"
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Mus musculus aspartyl beta-hydroxylase (ASPH) gene, exon 24 and
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Mus musculus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus

Dinchuk,J.E., Henderson,N.L., Burn,T.C., Huber,K., Ho.S.P.,

Link,J., O'Neil,K.T., Pocht,R.J., Scully,M.S., Hollis,J.M.,

Hollis,G.F. and Friedman,P.A.

Aspartyl beta -hydroxylase (Asph) and an evolutionarily conserved isoform of Asph missing the catalytic domain share exons with
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Submitted (25-JUL-2000) Applied Biotechnology, DuPont
Phermaceuticals Company, PO BOX 80400, Wilmington, DE 19880, USA
(bases 1 to 6024)
Henderson, N. L., Dinchuk, J. E., Burn, T. C., Hollis, G. F. and
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Henderson, N.L., Dinchuk, J.E., Burn, T.C., Hollis, G.F. and
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Mus musculus (house mouse)
                    Mus musculus (house mouse)
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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/produCt="asparty1 beta-hydroxylase 6.6 kb transcript"
/db xref="di:1187812"
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GDGDPVDDAKVLGIKERSPSERTPPPBAETHYDSDDRFFDLEGTWHEELDAABKLRK
GTGESVHTDDHSISTISETINAKYPOSPRAYGKAPQULDAERGRANGPYEPSEHEGV
EISDNTIDDSSIISETINAKYPOSPRAYGKAPQCEDDLAEKGRSNEVLRALITKOBLGYGTLLAG
PDAAPDIVKLSENTRKERSERQPTLGMRGBLITLQRLVQLFPSDTTLKNDLGYGTLLAG
NDSAKKYYERVLNVTPNDGFAKVHYGFILKAQNKISESIPYLKGIESODPGTDDGRF
YFHLGDAMQRVGNKARYKWYELGHRRGHFASVWQRSKNEVTRE
LVKSLEBNWKLIRDGLAMVNDKAKGHFLASVWQRSKNEVTRG
APKTCALLEKESETTGCRRGOIKYSINHPGTHWPGTTNGRLRMHGGLVIPFEGGK
APKTCALLEKESETTGCRRGOIKYSINHPGTHWPGTTNGRLRMHGGLVIPFEGGK
APKTCANETTWEEGGKVLIPDDSFEHEVWQDASSFRLIFIVDVWHPELTFDQQRRSLPAI"
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Mouse DNA sequence from clone RP23-152A20 on chromosome 4, complete
Dinchuk, J. B., Henderson, N. L., Burn, T. C., Huber, R., Ho, S. P.,
Link, J., O'Neil, K. T., Focht, R. J., Scully, M. S., Hollis, J. M.,
Hollis, G.F. and Friedman, P. A.
Aspartyl beta - hydroxylase (Asph) and an evolutionarily conserved
isoform of Asph missing the catalytic domain share exons with
                                                                                                                                                                                                                                                              Direct Submission
Submitted (26-UTL-2000) Applied Biotechnology, DuPont
Submitted (26-UTL-2000) Applied Biotechnology, DuPont
Pharmaceuticals, P.O. Box 80400, Wilmington, DE 19880-0400, USA
Location/Qualifiers
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. 7.3e-07;
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/chromosome="8"
/map="8q12 at STS WT-11767"
/tissue_type="liver"
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llarity 100.0%; Pred. No. 7.3
Conservative 0; Mismatches
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'strain="BALB/c"
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AL671970.8 GI:46878903
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/gene="Asph"
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/gene="Asph"
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'gene="Asph"
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mis musculus aspartyl beta-hydroxylase cardiac isoform 1 (Asph) Appliced. Application 1 (Asph) AP289491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sangcr.ac.uk/Projects/C elegans/wormpep This sequence http://www.sangcr.ac.uk/Projects/C elegans/wormpep This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

RP23-152A20 is from the RPCI-23 Mouse BAC Library
constructed by the group of Pieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence from the Mouse Genome Sequencing Consortium whole genome shoquence from the whole been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

Location/Qualifiers
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Chordata, Craniata, Vertebrata, Buteleostomi,
Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                    Submitted (29-APR-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Apr 29, 2004 this sequence version replaced gi:21531211.
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Best Local Similarity 100.0%; Pred. No. 7.5e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0;
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Contact: humquery@sanger.ac.uk
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/clone_lib="RPCI-23"
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ORGANISM

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Carminci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McSwan, P.J., Mullahy, S.J., Malek, J.A., Gunaratne, P.H., Richards, S. Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Sheychenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Snailus, D.E., Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

E. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 12746447.
Location/Qualifiers
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YGELSFLYDIMTPFEMLBEBEBEBESTADGVDGTSQNBGVQGKTCVILDLHNQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg, R. Strausberg, R. Strausberg, R. Strausberg, R. Strausberg, R. Submission Submission (03-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: MGC help desk
Bmall: oggapbe-r@mall.nih gov
Tissus Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Michael Brownstein / Ted Usdin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
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BC061098 GI:38173948
MGC
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

I (bases I to 1763)

Strausberg, R.L., Feingold, E.A., Grouse, D.H., Derge, J.G.,

Riausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altechul, S.F., Zeeberg, B., Buetow, K.H., Scheefer, C.F., Bhat, N.K.,

Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Heish, F.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
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                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammaliai, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Musi 1 (Dases 1 to 524)
Dinchuk, J.E., Henderson, N.L., Burn, T.C., Huber, R., Ho, S.P.,
Link, J., O'Neil, K.T., Pocht, R.J., Scully, M.S., Hollis, J.M.,
                                                                                                                                                                                                                                                            Aspartyl beta -hydroxylase (Asph) and an evolutionarily conserved isoform of Asph missing the catalytic domain share exons with
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/gene="Asph"
ppriced" asparaginyl beta-hydroxylase; AspH; alternatively
spliced"
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Submitted (25-JUL-2000) Applied Biotechnology, DuPont
Pharmaceuticals, P.O. Box 80400, Wilmington, DE 19880-0400, USA
Location/Qualifiers
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Dinchuk, J.E., Henderson, N.L., Burn, T.C., Hollis, G.F. and
Priedman, P.A.
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Conservative 0, Mismatches 0, Indels
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, R., Farmer, A.A., Rubin, G.M., Hong, L., Stapleron, M., Soares, W. B., Bondldo, M. F., Casavanth, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Garninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McKarnan, R.J., Male, S., Garcia, M., Gay, L.J., Hulyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Fahey, J., Helton, E., Ketteman, M., Madan, A., Schmutz, J., Myr, Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Kzzywinski, M.I., Salska, U., Smailus, D.E., Butterfield, Y.S., Kzzywinski, M.I., Salska, U., Smailus, D.E., Grheroth, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC015281 2770 bp mRNA linear ROD 16-SEP-2003 Mus musculus aspartate-beta-hydroxylase, mRNA (cDNA clone IMAGE:4235968), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                          QAPEGADIQNYEDEYKEQIGSLLQESVHTDHDLEADGLAGEPQPEVEDFLTVTDSDDR
FEDLEPGTVHEEIEDTYHVEDTASQNHPNDMEEMTNEQENSDPSEAVTDAGVLLPHAE
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WFDLVDYEEVLGKLGVYDADGDGDFDVDDAKVLLGLKERSPSERTFPPEAETHAELEE
                    There is and Kim, D.H.
Hong, C.-S. and Kim, D.H.
Direct Submission
Submitted (05-SEP-2000) Life Science, Kwangju Institute of Science and Technology, Puk-gu, Oryong-dong, Kwangju S00-712, South Korea on Oct 29, 2001 this sequence version replaced gi:15824389.
Location/Qualifiers
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100.0%; Pred. No. 3.3e-05;
tive 0; Mismatches 0;
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/db_xref="GI:16507231"
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                                                                                                                                                                                            /organism="Mus musculus"
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/strain="BALB/c"
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Mus musculus aspartyl beta-hydroxylase (ASPH) gene, exon 3.
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Dinchuk, J. E., Henderson, N. L., Burn, T. C., Huber, R., Ho, S. P., Link, J., O'Neil, K. T., Focht, R. J., Scully, M. S., Hollis, J. M., Appartyl beta hydroxylaee (Asph) and an evolutionarily conserved isoform of Asph missing the catalytic domain share exons with
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Sciurognathi; Muridae; Musinae; Mus
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Submitted (25-JUL-2000) Applied Biotechnology, DuPont
Submitted (25-JUL-2000) Applied Biotechnology, DuPont
Pharmaceuticals Company, PO BOX 80400, Wilmington, DE 19880, USA
Location/Qualifiers
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fenderson, N.L., Dinchuk, J.E., Burn, T.C., Hollis, G.F. and
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2617 bp mRNA linear Mus muscalus cardiac junctate 1 mRNA, complete cds. AF302653.2 GI:16507230
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100.0%; Pred. No. 3.2e-05;
tive 0; Mismatches 0;
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                                                                                                                                                                 303 TTTGATGTGGATGATGCCAAAGTTTTATTAGG 334
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/db xref="taxon:10090"
1105. 1173
/gene="ASPH"
/number=3
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Mammalia; Eutheria; Rodentia; Scii
I (bases 1 to 2617)
Hong, C.-S. and Kim, D.H.
Cloning of mouse junctin homologs
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           /db_xref="CDD:pfam05279"
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Mus musculus
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                                                                                                   Best Local Similarity
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Length 2617;

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AL773548 198991 bp DNA linear ROD 01-OCT-2002 Mouse DNA sequence from clone RP23-70D2 on chromosome 4, complete
                    Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 2789)
Dinchuk, J.B., Henderson, N.L., Burn, T.C., Huber, R., Ho, S.P.,
Link, J., O'Neil, K.T., Focht, R.J., Scully, M.S., Hollis, J.M.,
Hollis, G.F. and Friedman, P.A.
Aspartyl beta -hydroxylase (Asph) and an evolutionarily conserved
isoform of Asph missing the catalytic domain share exons with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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Dinchuk,J.E., Henderson,N.L., Burn,T.C., Hollis,G.F. and
Friedman,P.A.
Direct Submission
Submitted (26-JUL-2000) Applied Biotechnology, DuPont
Pharmaceuticals, P.O. Box 80400, Wilmington, DE 19880-0400, USA
1. 2789
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/gens="Asparaginyl beta-hydroxylase; AspH;
/note-flumbug; asparaginyl beta-hydroxylase; AspH;
non-catalytic isoform; alternatively spliced"
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Local Similarity 100.0%; Pred. No. 3.3e-05;
Les 32; Conservative 0; Mismatches 0; Indels
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J. Biochi
J. Biochi
20564328
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/dhromosome="8"
/map="8q12 at STS WT-11767"
/issue type="liver"
1. 2789
/gene="Asph"
| . .174
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/mol_type="mRNA"
/strain="BALB/c"
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/gene="Asph"
2783. .2788
/gene="Asph"
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                                                                                                                        NUMBER OF STOREST OF THE NUMBER OF STOREST OF STATE OF ST
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 12746447
This clone has the following problem: The cds is short compared to the longest cds in the locus.

Location/Qualifiers

1. .2770
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/product="Asph protein"
/protein id="AAH152B1.1"
/db_xref="G1:15929716"
/db_xref="G1:15929716"
/db_xref="MG1:1914186"
/db_xref="MG1:191486"
/db_
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Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/clone="IWAGE:4235968"
/clsue=type="Kidney, normal. 5 month old male mouse."
/clone lib="NGI CGAP_Kid14"
/lab_host="DH10E"
/note="Vector: pCMV-SPORT6"
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db_xref="LocusID:65973"
db_xref="WGI:1914186"
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Best Local Similarity 100.0%; Pred, No. 3.3e-05;
Matches 32; Conservative 0; Mismatches 0; Indels
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/mol_type="mRNA"
/strain="FVB/N"
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gene="Asph"
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/gene="Asph"
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Buraryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleogtomi; Bukammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 919)
Jones, L.R., Zhang, L., Sanborn, K., Jorgensen, A.O. and Kelley, J. Jorgensen, A.O. and primary structure, and immunological characterization of the 26-kDa calsequestrin binding protein (junctin) from cardiac junctional sarcoplesmic reticulum 96 (1995)
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/db_xref="G1:11878122"
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/tb_xref="G1:11878122"
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/tb_yref="G1:1187812"
/tb_yref="G1:1
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Zhang.L. and Jones,L.R.

Direct Submission

Submitted (06-4M-2000) 47, Sigma Chemical Co., N-3, 3300 South
Second Street, St. Louis, MO 63118, USA

Location/Qualifiers
                                                                                                                                                                                                                                                  Submitted (26-UUL-2000) Applied Biotechnology, DuPont Pharmaceuticals, P.O. Box 80400, Wilmington, DE 19880-0400, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="BAH; asparaginyl beta-hydroxylase; AspH; alternatively spliced" /codon_start=1
                                                                                                              2 (bases 1 to 566)
Dinchuk,J.E., Henderson,N.L., Burn,T.C., Hollis,G.F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF221854 Mus musculus cardiac junctin mRNA, complete cds.
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/note="calsequestrin binding protein"
                 Chem. 275 (50), 39543-39554 (2000)
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100.0%; Pred. No. 0.00011;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="8q12 at STS WT-11767"
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/mol_type="mRNA"
/strain="BALB/c"
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/db_xref="taxon:10090"
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/chromosome="8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="heart"
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AF221854.1 GI:12655824
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Best Local Similarity
Matches 31; Conserva
                                                                                                                                                                                                Friedman, P.A.
                            J. Biol. 20564328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 10); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
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Mus musculus asparaginyl beta-hydroxylase cardiac isoform 2 mRNA,
partial cds; alternatively spliced.
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Dinchuk, J.E., Henderson, N.L., Burn, T.C., Huber, R., Ho, S.P., Link, J., O'Neil, K.T., Focht, R.J., Scully, M.S., Hollis, J.M., Aspartyl beta - hydroxylase (Asph) and an evolutionarily conserved isoform of Asph missing the catalytic domain share exons with
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                   Lovell, J.

Direct Submission
Submitted (01-0CT-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk (Clone requests: clonerequest@sanger.ac.uk
on Oct 2, 2002 this sequence version replaced gi:23395448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-70D2 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/clone_lib="RPCI-23"
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Location/Qualifiers
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                                          (bases 1 to 198991)
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ROD 02-FEB-2001

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Indels

Length 566;

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/procein_id="AANB7549.1"
/db_xref="G1:27261146"
/db_xref="G1:2726114
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Direct Submission
Submitted (12-JAN-2000) Life Science, Kwangju Institute of Science and Technology (K-JIST), Puk-gu, Oryong-dong, Kwangju 500-712,
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                                                                          Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1013)
Hong, C. and Kim, D.H.
Mouse junctin-1 mRNA
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Dinchuk, J. E., Henderson, N. L., Burn, T. C., Huber, R., Ho, S. P., Link, J., O'Neil, K. T., Focht, R. J., Scully, M. S., Hollis, J. M., Hollis, G. F. and Friedman, P. A.
Rspartyl beta -hydroxylase (Asph) and an evolutionarily conserved isoform of Asph missing the catalytic domain share exons with
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Submitted (26-JUL-2000) Applied Biotechnology, DuPont
Pharmaceuticals, P.O. Box 80400, Wilmington, DE 19880-0400, USA
Location/Qualifiers
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Dinchuk, J.E., Henderson, N.L., Burn, T.C., Hollis, G.F. and
Friedman, P.A.
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1.3%; Score 31; DB 10; Length 10
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 31; Conservative 0; Mismatches 0; Indels
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Acrganiam="Mua musculus"
Mol type="mRNA"
Strain="BALB(C"
db_xref="teaxon:10090"
fiseue_type="heart"
168. 791
Codon start=1
/product="junctin-1"
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Mus musculus
                           AF223413.1 GI:27261145
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19, C. and Kim, D.H.
                    VERSION
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GDGPPVDDAKVLLGGGGALAKRKKAKAKEPIKEELKKERGKAVPSKNEERRGKKK
GEDRGKGRKKPDSDTSOKASAAGKRDRDKEKASSDKSSKSKESWKKAVETKAVSSKVA
ARDKDRRGRSSSGHAHVSKENGQKRKN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Numerators Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buthoria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 98). Hong, C.-S. and Kim, D.H. Mouse junctin-2 mRNA. Unpublished 1 to 988) Hong, C. and Kim, D.H. Direct Submission Submitted (12-JAN-2000) Life Science, Kwangju Institute of Science and Technology (K-JIST), Puk-gu, Oryong-dong, Kwangju 500-712, and Technology (K-JIST), Puk-gu, Oryong-dong, Kwangju 500-712,
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Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 31; Conservative 0; Mismatches 0; Indels
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Mus musculus junctin-2 mRNA, complete cds.
AF223414
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/organism=Mus musculus"
/organism=Mus musculus"
/organism=Mus musculus"
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/db_xref="texon:10090"
/db_xref="texon:10090"
/cissue_type="heart"
/codon start=1
/codon start=1
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ROD 29-OCT-2001

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/translation="WaedKrakHgghKNGRRGGISGGSFFTWFWVIALLGVWTSVAVV
WFDLVDYEEVLGKLGVYDADGDGDFDVDDARVLLEGPGGLAKRTKKKGLKERSPSER
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EIEDTYHVEDTASQHHINDMEEMTRECENSPSEAVTDAGVLLPHAEEVRHQDYDEPV
YEPSEHEGVEISDNTIDDSSIISEEINVASVEEQQDTPPDT"
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*** SEQUENCING IN PROGRESS ***.
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1 (bases 1 to 158289)
Csuros,M. and Milosavljevic,A.
Pooled genomic indexing (PGI): mathematical analysis and experiment
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2 (bases 1 to 158289)
Milosavljevic, A., Sodergren, E., Csuros, M., Li, B., Jackson, A.R.,
Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L.,
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Hong, C.-S. and Kim, D.H.

Hong, C.-S. and Kim, D.H.

Birect Submission

Submitted (05-SEP-2000) Life Science, Kwangju Institute of Science and Technology, Puk-gu, Oryong-dong, Kwangju 500-712, South Korea Location/Qualifiers
                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. I (bases I to 2613)
Hong, C.-S. and Kim, D.H.
Cloning of mouse junctin homologs
Unpublished
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(in) Guigo, R. and Gusfield, D. (Eds.);
ALGORITHMS IN BIOINFORMATICS, SECOND INTERNATIONAL WORKSHOP, WABI
2002, ROME, ITALY, SEPTEMBER 17-21, 2002, PROCEEDINGS: 10-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                   AF302654 arnus 2637 bp mRNA linear Mus musculus cardiac junctate 2 mRNA, complete cds
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0.00012;
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251 TTTGATGTGGATGATGCCAAAGTTTTATTAG 281
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/protein_id="AAL09320.1"
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/mol type="mRNA"
strain="BALB/c"
/db_xref="taxon:10090"
120. 899
                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
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KERGKAVPSKNEERRQGKKEQEDRGKGRKKPDSDTSQKASAAGKRDRDKEKASSDKSS
KSKESWKKAVETKAVSSKVAARDKDRRGRSSSGHAHVSKENGÇKRKN"
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(2 (base)
(
                                                                                                                                                                                                                                                                                                                                                                           translation="MAEDKEAKHGGHKNGRRGGISGGSFFTWFMVIALLGVWTSVAVV
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

1 (bases 1 to 2432)

Hong, C.-S. and Kim, D.H.

Cloning of mouse junctin homologs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1733;
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Mus musculus cardiac junctate 3 mRNA, complete cds.
AF302655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.3%; Score 31; DB 10; Length 17
100.0%; Pred. No. 0.00012;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                          'note="calsequestrin binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47. .694
/codon_start=1
/prodouct="cardiac_junctate_3"
/protein_id="AAL09231.1"
/db_xref="GI:15824394"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 TTTGATGTGGATGCCAAAGTTTTATTAG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 TTTGATGTGGATGATGCCAAAGTTTTTTAG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 TTTGATGTGGATGATGCCAAAGTTTTATTAG 333
                                                                                                                          /map="8q12 at STS WT-11767"
/tissue_type="heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                            protein_id="AAG40812.1"
db_xref="G1:11878118"
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/strain="BALB/c"
/db_xref="taxon:10090"
/chromosome="8"
                                                                                                                                                                                                                                                                                                    product="junctin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                             codon_start=
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Best Local Similarity 100.
Matches 31; Conservative
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Amaratunga, H.C., Are, J. R., Ayele, N., Banks, T., Barbarla, J., Bankarla, J., Bankarla, J., Bankarla, J., Bankarla, J., Bimaga, K., Blankenburg, K., Bounin, D., Bouck, J., Burch, P., Burket, C., Briewa, M., Brown, B., Brown, M., Bryan, C., Carron, T.F., Carter, P., Burket, C., Burch, B., Chiu, D., Chowdhry, J., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Chowdhry, J., Christopoulos, C., Cleveland, C.D., Den, J. L., Ding, Y., Dinh, H.H., Douthwaite, K. J., Daraper, H., Duy, Y., Duhin, H.H., Douthwaite, K. J., Daraper, H., Duny, R. C., Emerling, S., Escencho, M., Faris, P., Ferraguto, D., Flagg, N., Ford, J., Foret, P. Farraguto, D., Flagg, N., Ford, J., Foret, P., Frantz, P., Gabisi, A., Gavara, W. Gunazatne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hant, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Herris, C., Harris, K., Hant, M., Houlowy, C., Hollins, B., Homai, F., Jondson, B., Jia, Y., Johnson, R., Jollyte, S., Toodah, F., Luaris, K., Karlows, B., Jia, Y., Johnson, R., Jollyte, S., Youdah, S., Garcis, A., Martindale, A., Landry, N., Liu, W., Liu, Y., Martindale, A., Martindale, A., Martindale, R., Mascher, S., Metsev, E., Massey, E., Mawhiney, E., Mitchell, T., Mohabbat, K., Mongomery, K., Pace, R., Stanley, H., Stone, R., Soarier, R., Tang, H., Tangs, H., Ta
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Center: Baylor College of Medicine
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* See http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: The contigs are based on the application

* of the PGI method using the Human genome (NCBI build 31)

* as the comparative genome.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: BCM
Wabb site: http://www.hgsc.bcm.tmc.edu/
Contact: hgac-halp&bcm.tmc.edu
Contact: hgac-halp&bcm.tmc.edu
Contert project information
Center project name: LBGJ
Center project name: CH250-269N19
Center clone name: CH250-269N19
Chemistry: Dye-primer Bodipy: inf$ of reads
Chemistry: Dye-primer Bodipy: inf$ of reads
Chemistry: Dye-primer Bodipy: inf$ of reads
Chemistry: Dye-primer Big Dye: inf$ of consensus quality: 9211 bases at least Q30
Consensus quality: 9211 bases at least Q30
Consensus quality: 10542 bases at least Q30
Amaratunge, H.C., Are, J.R., Ayele, M.
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COMMENT

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Bacare 1. C. 234548 Main, A., Adams, C., Alder, J., Alanzny, D. Marie, Metzker M. Lee., Abramzon, S., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebecht, V. Aoyagi, A., Ayodeli, M., Baca, E. Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Baca, E., Brown, M., Baldwin, D., Bandaranaike, D., Barber, M., Baca, E., Brown, M., Bilway, C., Burch, P., Burchl, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, R., Chen, R., Chen, Y., Chen, Z., Chu, J., Clackeland, C., Coxtell, R., Cox, C., Dunn, A., Durnh, H., Divyak, N., Delgado, O., Denson, S., Derman, C., Ding, Y., Dinh, H., Divyak, N., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Garcia, A., Garza, M., Gunzatue, P., Hauland, W., Hanil, C., Hamilton, K., Havlak, E., Geer, K., Gill, R., Garcia, A., Garza, M., Gunzatue, P., Haaland, W., Hamilton, C., Hamilton, K., Harlak, P., Hawes, A., Henderson, N., Hernandez, J., Hoellins, B., Howells, S., Hladun, S.L., Hodgson, A., Hoguson, P., Havelk, P., Hawes, A., Hamilton, C., Hamilton, K., Karpathy, S., Kelly, S., Kally, M., Lu, X., Ma, J., Lorensuhewa, L., London, P., London, B., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Marehwai, M., Liu, Y., London, P., London, E., Lu, X., Ma, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Mahemari, M., Mahula, P., Martin, R., Martin, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACU95635 234548 bp DNA linear HTG 09-MAY-2003
Rattus norvegicus clone CH230-8Kl, WORKING DRAFT SEQUENCE, 2
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 152289: contig of 158289 bp in length.
Location/Qualifiers
1...158289
/organism="Macaca mulatta"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.3%; Score 30; DB 2; Length 158289; Best Local Similarity 100.0%; Pred. No. 0.00043; Matches 30; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/db_xref="taxon:9544"
/cloine="CH350-869N19"
1. .158289
/note="assembly name:CH250-269N19.1B
CONFIDENCE:_0.83"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC095635.6 GI:30467118
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1310 AGGTCATATGAGAGGTTCCCTGCTTACCCT 1339
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AC095635/c
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organism="Rattus norvegicus"

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Worley, K.C.

Direct Submission

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department Submitted (17-SEP-2001) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Skat Genome Sequencing Consortium.

Direct Submission

Submitted (09-MAY-2003) Human Genome Sequencing Center, Department Submitted (09-MAY-2003) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 9, 2003 this sequence version replaced gi:24817791.

The Sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.Dgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold in the Atlas individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole senome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sned, A., Sorong, X.-Z., Sorolle, R., Sosa, J., Strong, X., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thingey, A., Trejos, T., Usmani, K., Valas, R., Warg, G., Wang, S., Warren, D., Waldron, L., Walker, B., Wang, J., Walliams, G., Wallson, R., Walker, B., Wang, J., Walght, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Wilderhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* to not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consensus quality: 222438 bases at least Q40 consensus quality: 2224642 bases at least Q30 consensus quality: 225972 bases at least Q30 Estimated insert size: 232080; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center code: BCW
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center clone name: CH230-8K1
------ Summary Statistics
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FEATURES

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Rattus.

Nexter, Mezker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, H., Bacae, E., Baden, H., Anyalebechi, V., Avyagi, A., Ayodeji, M., Baca, E., Baden, H., Anyalebechi, V., Avyagi, A., Ayodeji, M., Bacas, E., Baden, H., Banahmed, F., Bilan, D., Balber, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Eroun, M., Bryan, C., Burd, C., Barchell, K., Caderon, E., Carderon, E., Cardenas, V., Carter, C., Coyle, M., Cree, A., D'Souza, L., Cleveland, C., Cockreil, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, Draper, H., Dugan-Rocha, S., Dunn, A., Dutbin, K., Duhin, K., Draper, H., Dugan-Rocha, S., Dunn, A., Dutbin, K., Duval, B., Foster, M., Franandez, S., Finley, M., Flagg, M., Fothes, L., Foster, M., Franer, C., Evan, Garner, T., Garze, M., Gabisi, A., Gerk, K., Gabisi, A., Garle, M., Hamil, C., Hamilton, C., Hamilton, C., Harrandez, R., Haladm, S. L., Hodgson, A., Hogues, M., Hernandez, R., Haladh, P., Hawes, A., Henderson, M., Hernandez, M., Hernandez, R., Haladh, S. L., Hodgson, A., Hogues, M., Jackson, J., Jackson, L., Jacob, L., Jackson, M., Hamilton, K., Jackson, L., Jackson, L., Jackson, M., Harnandez, M., Mally, S., Khan, Z., King, L., Kowai, C., Kraft, C.L., Lebow, H., Lewis, L., Lulle, M., Mully, M., Liuly, M., Malloy, K., Martin, R., Martin, R., Martin, R., Mayun, Mayun, M., Mayun, M., Mayun, M., Mayun, Mayun, M., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL128U56 275547 bp DNA linear HTG 15-NOV-2002
Rattus norvegicus clone CH230-16O22, WORKING DRAFT SEQUENCE, 4
UNOCCERED DIECES.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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0.0015;
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1.2%; Score 29; DB
Best Local Similarity 100.0%; Pred. No. 0.00
Matches 29; Conservative 0; Mismatches
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                                                                                                 1. .1711
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PAT 27-SEP-2004

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H010058805 2013 bp DNA linear ROD 13-MAR-2001 Mus musculus aspartyl beta-hydroxylase (ASPH) gene, exon 15. AF289209
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Patent: WO 2004/0783-A 156 16-SEP-2004;
Eirx Therspeutics Ltd (IE)
Location/Qualifiers
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Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 2013)
Dinchuk, J.E., Henderson, N.L., Eurn, T.C., Huber, R., Ho, S.P.,
Link, J.G., O'Neil, K.T., Focht, R.J., Scully, M.S., Hollis, J.M.,
Hollis, G.P. and Friedman, P.A.
Rapartyl beta -hydroxylase (Asph) and an evolutionarily conserved
isoform of Asph missing the catalytic domain share exons with
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Henderson, N.L., Dinchuk, J.E., Burn, T.C., Hollis, G.F. and
                                                                                                                                                                                                                             1.2%; Score 29; DB 2; Length 275547; 100.0%; Pred. No. 0.0015; tive 0; Mismatches 0; Indels 0;
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20564328
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Sequence 156 from Patent WO2004078783.
CQ871665.1 GI:52745698
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26655. .267994
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Best Local Similarity 100.0
Matches 29; Conservative
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CQ871665/c
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Mirect Submission

Submitted (19-JUL-2002) Human Genome Sequencing Center, Department Submitted (19-JUL-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (Dasses I to 275547)

Rat Genome Sequencing Consortium.

Direct Submission

Numitted (15-NOV-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

ON Nov 15, 2002 this sequence version replaced gi:23665157.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig described individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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NOTE: This is a 'working draft' sequence. It currently consists of a contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct Submission
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Center: Baylor College of Medicine
Center code: BCM
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Worley, K.C.
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274459
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FEATURES

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Gaps

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Length 27;

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Unpublished
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250664
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TITLE
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Nuzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, H., Alsbrooke, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Pydogi, M., Baca, E., Baden, H., Benahmed, F., Bladain, D., Bandaranaike, D., Barber, M., Bara, E., Baden, H., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bardhin, D., Bandaranaike, D., Barber, M., Barnstead, M., Bandar, C., Barch, T., Blankenburg, K., Blyth, P., Brown, M., Baddark, C., Burch, P., Burchl, K., Calderon, E., Cardenas, V., Chen, Z., Chen, G., Chen, G., Chen, G., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cladaro, J., Denson, S., Deramo, C., Coyle, M., Cree, A., D'Souza, L., Delgado, O., Denson, S., Deramo, C., Bard, Y., Dhuh, H., Divak, B., Escotto, M., Baccetto, M., Escotto, M., Malloy, K., Martinez, E., Husch, M., Liu, Y., Liu, W., Martinez, M., Mantiagua, M., Martinez, M., Mathiney, S., Misch, M., Martinez, E., Machanier, M., Mantidar, M., Martin, M., Perez, M., Perez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCUSE 1/8

252366 bp DNA linear HTG 10-MAY-2003
Rattus norvegicus clone CH230-11D6, WORKING DRAFT SEQUENCE, 3
unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                      Direct Submission
Submitted (25-JUL-2000) Applied Biotechnology, DuPont
Pharmaceuticals Company, PO BOX 80400, Wilmington, DE 19880, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              1.2%; Score 27; DB 10; Length 2013;
100.0%; Pred. No. 0.019;
iive 0; Mismatches 0; Indels (
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AC096178.6 GI:30522511
HTG: HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                                                                                                                                               1. .2013
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/number=15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 AAAATTGAGGAAGCAGTGAATGCATTT 321
                                                                                                                                                                                                                                                                                                                                                                                                                              0.0ery Match 1.2%
Best Local Similarity 100.0
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus
Friedman, P.A
                                                                                                                                                        source
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AC096178
                                                                                                                     FEATURES
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KEYWORDS
SOURCE
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                                                               JOURNAL
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AL Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030 USA
Baylor Plaza, Houston, TX 77030 USA
On May 10, 2003 this sequence version replaced gi:24818276.
On May 10, 2003 this sequence consist assembled using Atlas and whole genome shorgun sequencing reads assembled using Atlas and whole genome shorgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shorgun sequence reads. Both be indicated in the feature table.
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneet, A., Sodergren, E., Song, Y.-Z., Sorelle, R., Sosa, J., Taylor, S. trong, R., Sutron, A., Svatek, A., Tabor, P., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Varay, V., Villasana, D., Walfkon, L., Walker, B., Wang, J., Wang, G., Warlson, R., Weczyk, R., Wooden, H., Worley, K., Williams, G., Willason, R., Waczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Weinstock, G. and Gibbs, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct, Submission
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NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department Submitted (17-SEP-2001) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (Dases 1 to 252366)
Rat Genome Sequencing Consortium.
Direct Submission
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Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center project name: GEPB
Center clone name: GR20-11D6
-------- Summary Statistics
Assembly program: Allas 3.0;
Consensus quality: 230832 bases at least Q40
Consensus quality: 235480 bases at least Q30
Consensus quality: 235460 bases at least Q30
Estimated insert size: 242518; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 248556: contig of 248556 bp in length

57 248656: gap of unknown length

57 250663: contig of 2007 bp in length

54 250763: gap of unknown length

54 252366: contig of 1603 bp in length.

Location/Qualifiers
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Center code: BCM
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Direct Submission

L Submission

Submission

Pharmaceuticals Company, PO BOX 80400, Wilmington, DE 19880, USA

Location/Qualifiers

I. 1209e" Genomic DNA"

Amol type="genomic DNA"

Ab xref="taxon:10090"

Number=22

Number=23

Number=23

Number=23
                                                                                                                  H010058810 12095 bp DNA linear ROD 13-MAR-2001 Mus musculus aspartyl beta-hydroxylase (ASPH) gene, exons 22 and
                                                                                                                                                                                                                                                            Mus musculus (house mouse)
Mus musculus
Musuculus
Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
(bases 1 to 1205)
Dinchuk, J.B., Henderson, N.L., Burn, T.C., Huber, R., Ho, S.P.,
Link, J., O'Nell, K.T., Focht, R.J., Scully, M.S., Hollis, J.M.,
Hollis, G.F. and Friedman, P.A.
Aspartyl Deta -hydroxylase (Asph) and an evolutionarily conserved isoform of Asph missing the catalytic domain share exons with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF016503
Rattus norvegicus procollagen C-proteinase enhancer protein (PCPE) mRNA, complete cds.
AF016503.1 GI:4102818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus.
1 (bases 1 to 1519)
Masda,M., Igarashi,H., Kano,M. and Yoshikura,H.
Proviral Integration into the Procollagen C-proteinase Enhancer
Protein Gene and Its Effects in Cultured Rat Fibroblasts Revealed
by an Excisable 'Hit-and-Run' Retroviral Vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 12095)
Henderson, N. L., Dinchuk, J. E., Burn, T. C., Hollis, G. F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.1%; Score 26, DB 10; Length 12095; Best Local Similarity 100.0%; Pred. No. 0.067; Matches 26; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 275 (50), 39543-39554 (2000)
20564328
         1809 GGCTTCATCCTGAAGGCACAGAACAA 1834
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AF289214.1 GI:11692643
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                                                                   RESULT 60
H010058S10
LOCUS
DEFINITION
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VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
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AF016503/c
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REFERENCE
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AUTHORS
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Mus musculus aspartyl beta-hydroxylase (ASPH) gene, exons 18 and
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Mus musculus (house mouse)
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dinchuk, J.B., Henderson, N.L., Burn, T.C., Huber, R., Ho, S.P.,
Link, J. O. Neil, K.T., Foote, R.J., Scully, M.S., Hollis, J.M.,
Hollis, G.F. and Friedman, P.A.
Aspartyl beta -hydroxylase (Asph) and an evolutionarily conserved
isocom of Asph missing the catalytic domain share exons with
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Submitted (25-JUL-2000) Applied Biotechnology, DuPont
Pharmaceuticals Company, PO BOX 80400, Wilmington, DE 19880, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Henderson, N. L., Dinchuk, J. E., Burn, T. C., Hollis, G.F. and
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1.2%; Score 27; DB 2; Length 252366;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 27; Conservative 0; Mismatches 0; Indels 0
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1.1%; Score 26; DB 10; Length 6629;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 26; Conservative 0; Mismatches 0; Indels (
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20564328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  170125 AAAAGAACAAATTCAGTCCCTTCTCCA 170151
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264. :906
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clone_end:T7
site:EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                            452 AAAAGAACAAATTCAGTCCCTTCTCCA 478
                                                                                                                                                                                        20540. 40522
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site:ECORI
end_sequence:BH340112"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1494 GCTTCATCCTGAAGGCACAGAACAA 1519
                                                                                                                                                                     end_sequence:BH340110"
20540. .40522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF289211
AF289211.1 GI:11692640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /number=18
4834. .4923
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/number=19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1764. .1862
/gene="ASPH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Friedman, P.A.
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                                                                                misc_feature
                                                                                                                                                                                      misc_feature
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H010058S07
LOCUS
DEFINITION
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ACCESSION

ORIGIN

ò g VERSION KEYWORDS SEGMENT

REFERENCE AUTHORS

MEDLINE PUBMED REFERENCE

AUTHORS

JOURNAL

TITLE

TITLE JOURNAL

FEATURES

exon exon

ORIGIN

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Gaps

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JOURNAL

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 to 2201 to 2201. Haire, R.N. and Litman, G.W. The murine form of TXK, a novel TEC kinase expressed in thymus maps to chromosome 5
                                                                                                                                                                                                                                                                                                                                                                            ERLLIROGEAKEGAFIVEDSRHIGSYTISVFTRARRHYÖSSIKHYÖIKKUDSGÖWYITER
HLEPSYDELIOYHOYRAAGIISRIRYPIGLGSCLPATSGESYEKWEIDESEJAFVKE
IGSGOFGVVHIGEWRAHIPVAIKAINEGSNSEEDFIERAKWMKLGHSRLVOLYGVCI
OOKDLYIYTERENGCLIDYILREKROOLOKALLLISMCODICEGMAYLERSCYIHRDLA
ARNCLVSSACVVKISDFGMARYVLDDEYISSSGAKFPVKWCPPEVFHRNKYSSKSDVM
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ORORPWRAKLMGKTOSNRGGYOPSKRKPLPPLPQEPPDERIOVKALYDFLPREPGNLA
LKRAEBYLILERCDPHWWKARDRFGNEGLIPSNYVTENRLANDBIYEWYHKNITRNOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Litman, G.W.

Direct Submission

Direct Submitted (19-OCT-1994) Gary W. Litman, Molecular Genetics, All

Submitted (19-OCT-1994) Gary W. Litman, Molecular Genetics, All

Children's Hospital, 801 6th Street S., St. Petersburg, FL 33701,

USA
                                                                                                                                                                                           function="tyrosine kinase"
note="txk belongs to tec family of tyrosine kinases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.0%; Score 24; DB 10; Length 1680; 100.0%; Pred. No. 0.83; ative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MMU16145 2204 bp mRNA linear Mus musculus tyrosine kinase Txk mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="thymus"
/dev_stage="5 week old"
1. .48
49 . 1632
/function="tyrosine kinase"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. 2204
/organism="Mus musculus"
/mol type="mRNA"
/strain="C57 BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mamm. Genome 6 (7), 476-480 (1995)
96059536
7579892
                                                                                                                                                                                                                                                                                   /protein_id="AAA86698.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:10090"
chromosome="5"
db_xref="taxon:10090"
chromosome="5"
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'tissue_type="thymus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 GAGCAGCGCAACAGCAGCAG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 GAGCAGCGGCAACAGCAGCAG 58
                                                                                    dev stage="adult"
...1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                codon start=1
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                                                                                                                                  'gene="txk"
                                                                                                                                                         84. .1667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U16145.1 GI:562124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.0ery Match
Best Local Similarity 100.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
SOURCE
ORGANISM
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CDS
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MMU16145/c
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DEFINITION
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                                                                                                                       gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / LTAIN 1 AL 1018-WINDAALTSLIGPFLLANVLPLARGOTPNYTRPVFLCGGDVTGES

GYVASEGFPNLYPPNKKCIWTITVPEGGTVSLSFRVPDMELHPSCRYDALEVFAGSGT

GYVASEGFPNLYPPNKKCIWTITVPEGGTVSLSFRVPDMELHPSCRYDALEVFAGSGT

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RMEKAQGTLTTPNWPESDYPPGISCSMHILDABNOVIMLTFCKFDVEBDTYCRYDSVS

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VERESAPSPEDDAGHGPGSRSDFWTGTSFKVRPPSKRFKVQPVEFDEGSPATQATPVAP

DAPSITCPRQYKRASGTLGSNFCSSSLVYTGTVKAMVRGPGGGLIVYVTSLLGYYKTGDL

DLPSPASGTSLKFYVPCKQMPPMKKGASYLLMGQVEENRGPILIPPESFVVLYRFUDD
           2 (bases 1 to 1519)
Masuda,M. and Igarashi,H.
Direct Submission
Submitted (30-JUL-1997) Department of Microbiology, Graduate School
of Medicine, The University of Tokyo, 7-3-1 Hongo, Bunkyo-ku, Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (09-JAN-1995) Connie L. Sommers, National Institute of Child Health and Human Development, National Institutes of Health, Bldg. 6B, Rm. 28210, Betheeda, MD 20892, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        product="procollagen C-proteinase enhancer protein"
(protein_id="AAD01592.1"
db_xref="G1:4102819"
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1.0%; Score 24; DB 10; Length 1519;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                       1. .1519

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/strain="F344"

/db xref="taxon:10116"

/cell_line="Rat2"

/cell_type="fibroblast"

/dev_stage="embryo"

1. .1519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncogene 11 (2), 245-251 (1995)
95349947
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                                                                                                                                                  location/Qualifiers
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                   gene="PCPE"
                                                                                                                                                                                                                                                                                                                                                                                                              'gene="PCPE"
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                                                                                                                                    113, Japan
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MMU19607/c
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Gaps . 0 ROD 12-OCT-1995

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Mus musculus (house mouse)

SM Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

1 (bases 1 to 2342)
Nakayama, H. and Fulita, Nonoguchi, K., Arii, S., Purutani, M., Kaneko, Y.,
Enhanced expression of multiple protein tyrosine kinases in the
mouse regenerating liver: Isolation of PTK.RL-18, a novel
cytoplasmic tyrosine kinase gene of Tec PTK family
L Unpublished
S Higgashiteuli, H.
S Higgashiteuli, H.
        /translation="MILSSYSSPQSVLCCCCRCSVQKRQVRTQISLSREEELSEKHS
QRQRPWRAKLMGKTQSWRGGVQPSKRRELPPLQPEPDEEL VQYKLYPELPREPGNLA
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BRLLRQEAKEGAFIVRDSRHLGSYTISVFTRARRHTQSSIKHYQIKKNDSGQWYITER
HLFPSVPELLQYHQYNAAGLISRLYPPTGLGCSGTCPATGSFSTEKWEIDPSELAFVKE
IGSGQPGVVHLGSFRAHIPVAITSRLKSWSEEDFIERAKVMMKLSHSRLVQLYGVCI
QQKPLYIVTEFMENGCLLDYLRERKGQLQKALLLSMCQDICEGMAYLERSCYIHRDLA
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SFGYLLMWEVFTGGMPFENKSNLQVVVBAISGGFRLYRPHLAPWITYRVWYSGWHESPY
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Mus musculus PTK-RL-18 mRNA for protein tyrosine kinase, complete
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0.83;
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                                                                                                                                                                                                                                                49. .1629
/gene="KLK"
/product="resting lymphocyte kinase"
/standard name="protein tyrosine kinase"
/evidence=experimental
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1. .2342
/organism="Mus musculus"
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/clone_lib="Uni-Zap XR"
/dev stage="adult"
1. 2342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  evidence=experimental
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/db_xref="taxon:10090"
/clone="ptk-18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=experimental
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/gene="RLK"
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D43963.1 GI:604883
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MUSPTKRL18/c
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/product="Txk"
/product="Txk"
/product="Txk"
/product="Txk"
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/db xref="G1:562125"
/translation="MILSSYSSFOSYLCCCCRCSYOKROVRTOISLSRBEELSEKHS
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LKRAREFILILERCDPHWRARDRFGREGILEBNYTEARRHTOISTKWDSGYNITER
ERLIAGBAKEGAFIVRDSRHLGSYTIGSYFTARRHTOSSITHYTOXIKNDSGYNITER
HEPPSYPELIOYHOVRHLGSYTIGSYFTARRHTOSSITHYTOSSITHYTOYT
GREFFLOYHOLGBWRAHIPVAIKAINESYLGSTLGASTGSFSYEWEIDPSELAFVKE
IGSGQFGYVHLGBWRAHIPVAIKAINEGSMSEEDFIEEAKVWMKLSHSRLVQLYGVCI
QQKPLYIVTERRNGGCLLDYLERRRGGOLGAALLLSWOODICGRAANTLERGYTHRDLA
ARNCLVSSACVVKISDEGRARYVLDDEYISSSGAKFPVKWGOPEVPHFRKYSSKSDVW
SFGTAMEVPTEGRAPFENKSNLQVVEAISGGFRLYRPHLAPMTIYRVWYSCWHESPK
GRPTFALLQVLTEIAFTW"
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Mus cookii resting lymphocyte kinase (RLK) gene, complete cds.
L35268
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Hu, Q., Davidson, D., Schwartzberg, P. L., Macchiarini, F., Lenardo, M. J., Bluestone, J. A. and Matisi. A. Identification of RIK, a novel protein tyrosine kinase with predominant expression in the T cell lineage J. Biol. Chem. 270 (4), 1928-1934 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="resting lymphocyte kinase"
note="predominant expression in T cell lineage; protein
yrosine kinase"
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Original source text: Mus cookii (clone K9A) tetus thymus cDNA to
mRNA.
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protein tyrosine kinase; resting lymphocyte kinase.
Mus cookii (Cook's mouse)
Mus cookii
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protein id="AAA67039.1"
/db xref="GI:623443"
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/mol_type="mRNA"
/db_xref="taxon:10098"
/clone="K9A"
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evidence=experimental
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dev stage="tetus"
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1. .2221
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/gene="RLK"
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/gene="RLK"
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Gaps

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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomyceteles; Dipodascaeae; Yarrowia.

Saccharomycetales; Dipodascaeae; Yarrowia.

CB bion,B., Sherman,D., Fischer,G., Durrens,P., Casaregola,S., Iafontaine,I., De Montigny,J., Marck,C., Neuveglise,C., Talla,E., Goffard,N., Frangeul,L., Aigle,M., Anthourad,V., Babour,A., Barbe,V., Barnay,S., Blanchin,S., Beckerich,J.M., Beyne,E., Goffard,C., Rolarwar,A., Despons,L., Fabre,B., Fairhead,C., Ferry-Dumazet,H., Groppi,A., Hantraye,F., Hennequin,C., Jauniaux,N., Joyet,P., Kachouri,R., Kerrest,A., Koszul,R., Janniaux,M., Joyet,P., Kachouri,R., Kerrest,A., Koszul,R., Jemaire,M., Lesur,I., Ma,L., Muller,H., Micadd,J.M., Nikolski,M., Oztas,S., Ozier-Kalogeropoulos,O., Pellenz,S., Potier,S., Richard,G.F., Straub,M.L., Sulleau,A., Swennen,D., Tekaia,F., Kachouri,R., Scandou-Mayer,M., Zivanovic,I., Bolotin-Fukuhara,M., Thierry,A., Bouchier,C., Caudron,B., Scarpelli,C., Gaillardin,C., Weissenbach,J., Wincker,P.
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Yarrowia lipolytica chromosome F of strain CL1B99 of Yarrowia
                                                         LOCUS CR382132 Accession CR382132
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Yarrowia lipolytica CLIB99
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Pred. No. 0.86;
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1.0%; Score 24; DB 2; Length 110000;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 24; Conservative 0; Mismatches 0; Indels 0.
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100.0%; Pred. No. 0.83;
ive 0; Mismatches 0; Indels (
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                                                                                                          product="protein tyrosine kinase"
protein id="BAA07900.1"
db_xref="G1:604884"
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100.0%; Pred. No. 0.80
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/gene="PTK-RL-18"
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Continuation (3 o
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AC013623 2
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Complement (19703. 20034)

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Clocus tag="YALIOPROIT'6g"

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Complement (19703. 20796)

Jocus tag="Interpretation product; similar to DEHAOG03828g

Debaryomyces harenii IPP 785.1 and sp|P20107

Saccharomyces cerevisiae YMR245c ZRC1 zinc- and cadmium

Codon start=1

/procein id="Cag77609.1"

/db_xref="Interpoint tag to product t
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KGLSTFMERMLETSALIKSATDKSLIIIDELGRGTSTYDGFGLAMAISEHIVKGNCFS
MFATHFBELTELAKEHPDRVDNLHAVAHVGESSDDITLLYKVVPGVSSKSYGTHVAEV
VKPPTKVNMAKRAGELDDVNSGTOGKKYASEDLVAGNKLLKEILTEWKSQIKGDEV
DGASQLLKTVVDKYKTQMEQNVFINDALASL"
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GSSNNAVDLAVCVCIVKYGKPGETELEITWSSPRELYYKKTYNVIKELSSYLASPYTEL
QDFATQFGSELFKY1SESLEBEGVPVLLTFULPSFRAYELNPVAPDTQKRIPPLDLELP
PELEQTLEVEFSDIEDEEVYVEEEFTPQFASTVSGVQKESLLDARKERLEKQKDDPFY
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Socciaromyces cerevisiae ORF YPLI95W Alpha/gamma adaptin, start by similarity"
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Zebrafish DNA sequence from clone DKEY-287H22 in linkage group 7, complete sequence.
BX663616
BX663616.13 GI:47522521
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Pred. No. 0.86;
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/ trainslation="MENDLINEPREAHGEDRYAGLICOVGSDLECALCOSIMEVPEVLD
/ CTATACLE = "ULL FIG. / ILEMBLINGUE # / "
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CGWWVNDGSGREAAAE] RYDYDEDEBESDSRQPGEDISDYEDGGFWYDDDSDDGGDPTG
DVTILSDSQASSPAPTSTYVQTNDSDLDSEDSDCHFYRKAGTSTYTDDSDDDGUCPR
RKHKIMSDSEDDHPAVESBREKGRRIFEDSSEDDSDCHOPPREKKRGTSTYTDSSDDDGUCPR
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/ Locus trad="YALIOFOOLSG" . 18501)
/ Locus trag="YALIOFOOLSG" . 18501)
/ Locus trad="YALIOFOOLSG" . 18501)
/ Locus trad="YALIO
                                                                                 Genoscope.
Direct Submission
Submitted (01-JUL-2004) Genoscope - Centre National de Sequencage :
Submitted (01-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex -FRANCE (B-mail : seqrefégenoscope.cns.fr -
Whe : www.genoscope.cns.fr |
This sequence is unfinished. Sequencing was performed at Genoscope and annotations were obtained by the genolevures Consortium.

Location/Qualifiers
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complement(13437. .14069)
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chromosome="F"
Nature 430 (6995), 35-44 (2004)
                                                             (bases 1 to 4003362)
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ORGANISM

KEYWORDS SOURCE

AUTHORS

JOURNAL

COMMENT

REFERENCE

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AL Submitted (20-10N-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBN0 15A, UK. E-mail enquiries:
Zifish-help@sanger.ac.uk Clone requests: clonerequestosanger.ac.uk
Zifish-help@sanger.ac.uk Clone requests: clonerequestosanger.ac.uk
Zifish-help@sanger.ac.uk Clone requests: clonerequestosanger.ac.uk
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with that source databases:
Em., EMBL, Sw., SWISSPROT; Tr., TREMBL, WP., WORNPEP; Information
on the WORNPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep CH211-225J17 is
from a CHORI-211 BAC library
WHOSTOR: PARRARACI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

This sequence is the entire insert of clone CH211-225JJT The true right end of clone CH211-23JILB is at 96893 in this sequence. Clone CH211-23JILB is at 96893 in this sequence. Clone CH211-23JILB is at 96893 in this sequence. Clone-darived Zebrafish pUC subclones occasionally display inconsistency over the length of mononuclectide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, Washu). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml
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1145. 1207
/note="CR1-1" DR repeat: matches 4919. .4981 of consensus"
1203. .1268
                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 192578)
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/note="Dr000087 repeat: matches 957. .1326 of
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note="19.0 copies 3 mer TAA 114% conserved"
.114. .1127
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/mol_type="genomic DNA"
/db_xref="texon:7955"
/clone="CH211-225917"
/clone_lib="CHORI-211"
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Contact: zfish-help@sanger.ac.uk
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                                                             HTG; zinc finger.
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AUTHORS
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 10); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SW:SSPROT; Tr:, TREMBL; Wp:, WORNPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived zebrafish puc subclones occasionally display inconsistency over the length of mononuclectife A/T runs and conserved in repeats. Where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-287H22
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Zebrafish DNA sequence from clone CH211-225J17 in linkage group 7
Contains part of a novel gene for a zinc finger protein, complete
                                                                                                                                                                                                                                                                                                                       Submitted (19-MAY-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Clone nequests: clonerequest@sanger.ac.uk Clone version replaced gi:47109759.
                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
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Contact: zfish-help@sanger.ac.uk
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/db_xref="taxon:7955"
/clone="DKEY-287H22"
/clone_lib="DanioKey"
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                                              Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                               Submission
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/note="DNA11TA1_DR repeat: matches 1. .186 of consensus"
complement(4960. .5090)
/note="Accombat1 repeat: matches 751. .876 of consensus"
complement(5134. .5259)
/note="DNA11TA1_DR repeat: matches 1. .130 of consensus"
                                                                                                                                              659. .1731
note="Dr000067 repeat: matches 207. .288 of consensus"
                               matches 135. .196 of consensus"
matches 776. .842 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="Dr000009 repeat: matches 770. .857 of consensus"
                                                                                                                                                                                                                                                                                                      note="HATI_DR repeat: matches 575. .647 of consensus"
1.03. __200__
1.03. __200__
1.03. __201_
1.04. __HATI_DR repeat: matches 555. .660 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408. .3448
note="HAT1_DR repeat: matches 577. .617 of consensus"
1456. .3467_
note="2.0" copies 6 mer AAACAG 24% conserved"
            complement (1214. .1275)

Jobce="Dr000340 repeat: matches 135. .196 of consensur complement (1272. .1327)

Inote="Pr000403 repeat: matches 1. .66 of consensus" complement (1369. .1617)

Jobce="Dr000262 repeat: matches 5. .284 of consensus"
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note="Dr000236 repeat: matches 358. .433 of consensus
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                                                                                                                                                                                                                                                                                                                                                      371. .3442
note="Dr000309 repeat: matches 2. .69 of consensus"
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/note="2.5 copies 4 mer ACAA 20% conserved"
                                                                                                                                                                                                                            copies 8 mer TTTAAAGA 26% conserved"
                                                                                                                                                                                            copies 6 mer TTAGTA 24% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="7.0 copies 2 mer TC 28% conserved 063. .3074 note="2.4_copies 5 mer ATATG 24% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="2.2 copies 5 mer AATAA 22% conserved"
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                                                                                                                                                                                                                                                           copies 4 mer AGAT 22% conserved"
                                                                                                                                                                                                                                                                      017. .2011
note="3.8 copies 4 mer CAGG 30% conserved"
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                                                                                                             1620. .1631
/note="12.0 copies 1 mer T 24% conserved"
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note="13.0 copies 1 mer T 26% conserved"
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note="22.0 copies 1 mer T 44% conserved"
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/note="2.8 co
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/note="7 ^
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note="2.8 c
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note="2.0 c
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note="8.5 co
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note="2.5 c
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HTG; HTGS_ACTIVEFIN.
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
HTG musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 222930)
                                                                                                                                                                                                                                         consensus,
                                                                                                                                                                                   7336. .8045
/note="Dr000209 repeat: matches 1. .678 of consensus"
8045. .8138
/note="Dr000364 repeat: matches 86. .180 of consensus"
                                                                                                                                                7250. .7336
/note="Dr000364 repeat: matches 4. .90 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DR1 repeat: matches 41. .221 of consensus"
                                                                                                                                note="TDR19 repeat: matches 198. .303 of consensus"
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/note="2.8 copies 4 mer CTTC 22% conserved"
10867. .10885
/note="3.2 copies 6 mer ACTGTA 29% conserved"
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6238. .6253
/notes 16.0 copies 1 mer A 32% conserved"
6626. .6635
/notes 2.5 copies 4 mer GAAT 20% conserved"
6738. .6760
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uplement(8972. .9131)
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                                                                                 6738. .6760
/note="7.7 copies 3 mer TCC 39% conserved"
complement(7233. .7249)
                                                                                                                                                                                                                                                     189. .8203
note="15.0 copies 1 mer T 30% conserved"
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/note="2.4
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/note="2.2 cm
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/note="22.7 r
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/note="6.0 ~~
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/note="5.5 c
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/note="2.5 co
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'note="5.2 co
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note="6.5 co
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222930: contig of 27854 bp in length.

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Elizen, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Canarata, J., Campopiano, A., Charag, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Daaz, J.S., Dodge, S., Faro, S., Gonde, P., Fithugh, M., Gage, D., Galagan, J., Gardhan, S., Gardyna, S., Gord, S., Govette, M., Graham, L., Gardhan, S., Lamazares, R., Harford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Karatas, A., Karatas, R., Meltrim, J., MacGonald, P., Major, J., Marquis, N., Methews, C., MacGonald, P., Major, J., Marquis, N., Methews, C., Nordan, C., MacGonald, P., Major, J., Marquis, N., Methews, C., Nordan, C., Retar, M., McEwan, F., O'Donnell, P., O'Neil, D., Commo, J., Raymon, C., Reta, R., Rebeack, M., Riley, R., Rise, C., Rogov, P., Sancos, R., Sancos, R., Sancos, S., Schupback, R., Stange-Thoman, N., Stojanovic, N., Stojanovic, V., Topham, K., Travers, M., Travis, N., Ville, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Direct Submission

Lizect Submission

Shimitted (18-NOV-2001) Whitehead Institute/MIT Center for Genome Shireer, Submission

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s: gap of 100 bp
s: gap of 100 bp
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7: contig of 3639 bp in length
8: gap of 100 bp
8: contig of 5291 bp in length
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7: contig of 4328 bp in length
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Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
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of 3759 bp in length
100 bp
        Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 5, clone RP23-41509
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Birrem, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cook, P., Colangelo, M., Galge, D., Galagan, J., Gardyna, S., Ferrelata, P., FitzHugh, W., Galge, D., Galgan, J., Gardyna, S., Gord, S., Goyette, M., Graham, L., Grand-Pleare, N., Gande, S., Gord, S., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamata, A., Karatas, A., Kells, C., LaRocque, K., Lawazaes, R., Landers, T., Mardas, A., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Norbu, C., Norbu, C., Norbu, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Norbu, C., Norbu, C., Norbu, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Repack, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Rotta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Travers, M., Travers,
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Mus musculus chromosome 18, clone RP24-160112, complete sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 224556)
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Birran, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Anderson, S., Arachchi, H.M., Barna, N., Chang, J., Chang, J., Choepel, Y.
Boguelavkiy, L., Boukhalter, B., Carum, B., DeArellano, K.,
Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,
Farzeira, P., Fitzderald, M., Gage, D., Erickson, J., Faro, S.,
Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,
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/clone_lib="RPCI-23 Female Mouse BAC"
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Mus musculus chromosome 18, clone RP24-160I12
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0.87;
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Location/Qualifiers
1. .222930
/organism="Mus musculus"
                                                                                                                                 /mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="5"
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Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J. Nguyen, C., Nicol, K., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Nicol, K., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Retrach, P., Rise, C., Rogov, P., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Schauge-Thomann, N., Scojanovic, M., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Voung, G., Zainoun, V., S., Vviel, R., Tarvers, M., Nuran, D., Young, G., Zainoun, V., Sembek, L., Zimmer, A. and Zody, M. Direct Submission at Cartes, Cambridge, MA 02141, USA (basein) at Cartes, Street, Cambridge, MA 02141, USA (basein) at Cookers of Collymore, A., Cook, A., Corum, B., Dearellan, N., Barna, N., Barna, N., Barna, M., Barna, M., Barna, M., Chang, J., Chopel, Y., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diad, J., S., Dodde, D., Galagan, J., Gardyna, S., Kanat, A., Karatas, A., Katatas, A., Mabbitt, R., MacLean, C., Liu, X., Liu, X., Lui, A., Mathews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Marna, V., Murphy, T., Naylor, J., Meldrim, J., Meneus, L., Mihova, F., Marby, T., Marlor, J., Maler, M., Mathews, C., McCarthy, M., Maler, M., Marche, J., Marlor, J., Mihova, F., Marby, T., Marlor, J., Maler, M., Mathews, C., McCarthy, M., Maler, M., Maler, M., Mathews, C., McCarthy, M., Maler, M., Maler	Nguyen,C., Nicol,R., Norbu,C., O'Comnor,T., O'Donnall,P., Nguyen,C., Nicol,R., Norbu,C., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pietre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Steae,C., Sochauer,S., Schauer,S., Schauer,S., Schauer,S., Schauer,S., Schauer,S., Schauer,S., Subbs,M., Stange-Thoman,N., Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataramann,V.S., Viel,R., Volk,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M. Direct Submission L. Submission Submission Research, 320 Charles Street, Cambridge, MA 02141, USA S. Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,M., Arachofi,H.M., Barna,N., Basien,V., Bloom,T., Boukhgalter,B., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., Dooley,R., Dorris,L., Erickson,J., Raro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Kamat,A., Karatas,A., Kalls,C., Lander,T., Johnson,R., Jones,C., Kamat,A., Karatas,A., Rells,C., Lander,T., Levine,R., Lindblad-Toh,K., Liul,S., Mabbitt,R., Maclanh,C., Macdonald,P., Maior,J., Matthew,M.	Meldrim, J., Meneüs, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Naylor, J., Naylor, J., Naylor, S., Natol, R., Norbu, C., O'Connor, T., O'Connall, P., O'Connall, P., O'Connor, T., O'Connall, P., O'Connor, T., O'Connall, P., O'Connor, T., C'Connor, Walling RepeatMasker. Neb site: http://www-seq.wi.mit.edu Conter o'Conter o'Connor, T., C'Connor, T., C'Con
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Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M. Direct Submission
                                                                                                                                             Submitted (15-APR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 25, 2003 this sequence version replaced gi:30018220. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barran, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Bachelano, A., Campapiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farc, S., Goyette, M., Grande, Pierre, N., Gardan, L., Grand-Pierre, N., Gardyna, S., Ginde, S., Goyette, M., Grand, P., Carlan, L., Grand-Pierre, N., Jones, C., Karatas, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Lanccaky, J., Levine, R., Lid, C., Macdonald, P., Marquis, N., Matthews, C., McGarthy, M., McEwan, P., McRernan, K., Marphy, T., Naylor, J., Mguyen, C., North, C., Norman, C.H., Murphy, T., Naylor, J., Mguyen, C., North, C., Norman, C.H., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Zambek, L., Zimmer, A. and Zody, M., Young, G., Zainoun, J., Direct, Submission, M., Zembek, L., Zimmer, A. and Zody, M., Young, G., Zainoun, J., Direct, Submission, M., Willer, W., Will
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Birren, B., Nusbaum, C. and Lander, E. Mus musculus chromosome 5, clone RP23-6518
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                                                                                                                                                                                          Score 24; DB 10; Length 224556;
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                    28999; contig of 28999 bp in length 29099; gap of 100 bp 36806; contig of 7707 bp in length 36806; gap of 100 bp 45591; contig of 8585 bp in length 48570; contig of 8079 bp in length 48770; gap of 100 bp 52331; contig of 3561 bp in length 52431; gap of 100 bp 67933; contig of 15502 bp in length 567933; contig of 15502 bp in length
                                                                                   Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L11591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 bp
of 11546 bp in length
100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig of 67278 bp in length
gap of 100 bp
contig of 41535 bp in length
gap of 100 bp
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82182 bp in length
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                                           Center code: WIBR
Web site: http://www-seg.wi.mit.edu
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100.0%; Pred. No. 0.87;
tive 0; Mismatches
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Seguence 127 from Patent WO2004078783.
CQ871636
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contig of
gap of 100
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                                                                                                                            Center project name: L115
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                                                                                                                       Murphy, F.J., Sheehan, D.E., Keating, K.E., Hayes, I.E. and Seera, L.E. Enzymes involved in apoptosis
Patent: WO 2004078783-A 127 16-SEP-2004;
Eirx Therapeutics Ltd (IE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 129S1/SvImJ, C3H/HeJ, and BALB/CByJ. The WGS reads were placed uniquely on the MGSCv3 CS7BL/6J assembly and SNP detection was carried out by SSAHA-SNP. 225,000 reads were annotated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 595)
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome
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1.0%; Score 23; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 23; Conservative 0; Mismatches 0; Indels
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320 Charles Street, Cambridge, MA 02141, USA
781: 6172521477
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                                         synthetic construct
synthetic construct
other sequences; artificial sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: kersil@genome.wi.mit.edu
Primer A: None
Primer B: None
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Mus musculus
  CQ871636.1 GI:52745669
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G94809.1 GI:22745565
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AUTHORS
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G94809/c
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AUTHORS
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Query Match 1.0%; Score 23; DB 11; Length 595;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps
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Search completed: March 25, 2005, 20:35:15 Job time : 9731 secs This Page Blank (uspto)

us-09-436-184-3.oligo.rst

CN274513 170006000 BP338261 BP288261 BQ889709 AGENCOURT BQ722578 AGENCOURT	BU132666 AU132666	BUS 228.06 AGENCOURT BF962729 QV2-NN004 BE935834 QV2-NN004 CN368827 170004243	AL700393 DKFZp686K BU502544 AGENCOURT AL120973 DKFZp762H CNAR1470 PW08P06 V	EF943222 QV2-NN004 CN481475 hw08b10.y	AU138660 AU138660 BQ318605 CM0-CT054 BQ278505 AGENCOURT	BF962946 QV2-NN004 BQ639558 hel7b04.y	CN483754 hw36h12.y	BQ340475 QV2-NN200 BQ339559 QV2-NN004 BQ223755 AGENCOURT	BI035330 QV2-NN200 BE084010 PM0-BT065	BU838423 AGENCOURT CN368831 170006008	CA311352 01-CF-FN0 CN368826 170004243 BE876059 601485742	AI267311 aq63e03.x CN368818 170006000	CN481268 hw05d04.y AL694159 DKFZD313D	AY405268 Pan trogl BX111251 BX111251	CF136513 UI-HF-BNO BG170148 602321860	CR630295 DKFZp4691 CR559422 DKFZp4681	CN482623 hw22f04.y CN368828 170004243	BE018154 bb76a02.y BM785890 K-EST0064	AV751514 AV751514 CDE12002 ACENCOME	BM462707 AGENCOURT	BU158882 ATTOURS	CR769476 DKFZP469H	AI652752 wb62d01.x BX374107 BX374107	T69872 yc18e11.rl	BG701542 602682786	BG332543 602433630	BI193485 602947432 BG977347 CM1-CT003	CB26568 1004563 H	BF154495 MR0-BN011	BF911695 QV1-UT009 BI546417 603188718	BU543358 AGENCOURT BU542964 AGENCOURT	CF619299 AGENCOURT AW994191 RC3-BN003	901655209 67799159
	BU19074 AU13266		1 AL700393 5 BU502544 1 AL120973 7 CN481470					5 BQ340475 5 BQ339559 5 BQ223755																								CF619299 AW994191 BC166775	
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Lu	nucleic search, using sw model	March 25, 2005, 16:47:45 ; Search time 6778 Se (without alignments 13051.248 Million c	US-09-436-184-3 2324 1 cqqaccqtqcaatqqcccaqcttqqqaaqtcto	NUC	dapup oo.o , dapext oo.o 34239544 segs, 19032134700 residues		hits satisfying chosen parameters:	length: 0 length: 200000000		ES.		4: 95 est 3: * 5: gb est 4: *		8: gb_gss1:* 9: gb_gss2:*	is the number of results predicted by ch	greater than or equal to the score of the result bein derived by analysis of the total score distribution.	SUMMARIES		Match Length DB ID	2126	1085 5	782 7	918 729 7	868 5	583 5	651 2	1011 5	581 5	765 6	517 5 721 4	711 7 868 5	20.5 520 7 CN368829 19.8 770 7 CN368823 19.7 689 4 DCT20020	n 0 0
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404 4 BG979400 BG979400 CM4-CN00 S4176259 EG979400 CM4-CN00 S64 6 CD675871 E829D12. EG675871 E921D12. EG675871 E921D12. EG675871 E921D12. EG675871 E920D12.	ò a ò	ି ପୁ	, qa ko	· 6	95 Q	& 43	8 S	% ଶ	상 점	% व	& 43	දු පු	& <u>8</u>	\$ A 6	Š A 5	∂ 6 €	දි දි	& &	ò
RESULT 1 AV405267 LOCUS DEFINITION HOME DEFINITION ANAH VERSION ANAH CORGANISM HOME BUKK BUKK BUKK BUKK BUKK BUKK BUKK BUK	5 9.7 404 4 BG979400 BG979400 CM4 2 9.6 549 1 AA176259 AA176259 Zp2 1 9.5 504 6 CD675871 CD675871 f82	ALIGNMENTS	AY405267 N Homo sapiens ASPH gene, VIRTUAL TRANSCRIPT, partial sequence,		GSS. Homo sapiens (human) SM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel	Mammalia; Eutheria; Primates; Catarrhini; Homini 1 (bases 1 to 2126) Clark, Glanowski, S., Nielson, R., Thomas, P., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F.,	<pre>Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthol gene trios</pre>			AL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and orderin them based on alignment.	rce		77.6%; Score 1803; DB 9; Length 2126; Similarity 100.0%; Pred. No. 0;	1903; COMBELTACIVE V, MISHACCAGAGACCAGAAAGAGAGACTCGCCACAAAAAGAAGAGACTCACACAAAAAAGAAGAGATCTACAGAGCCAGCAGAAGAGCCAGAAGAGAGCTACACACAAAAGAAGAGATCTACAGAAGCCAGCAGCAGCAGCAGAAGAGAGCCAGAAGACACACACAAAAAA	CTGAGCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACCCCAGAATATCGAAGAAA	aagaacaaattcagtcccttctccatgaaatggtacacgcagaacatgttgagggagaag 	ACTTGCAACAAGAAGATGGACCCACAGGAGAACCACAACAAGAGGGATGATGAGTTTCTTA 	TGGCGACTGACTGTAGATGATAGATTTGAGACCCTGGAACCTGAAGTATCTCATGAAGAAA TGGCGACTGACTGTAGATGATGATTTGAGACCCTGGAACCTGGAAGTATCTCATGAAGAAA	100000000000000000000000000000000000000

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BX459083 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE012YB13 - FRIME, mRNA sequence.
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Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1085)
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                          121 AAGTTAAGAAAAAAAAGCCTAAACTTTTAAATAAATTTGATAAGAACTATTAAAGCTGAAC
                                                                                                                                                                                                                                                                                                                           1045 TTGATGCTGCAGAAAAACTCCGTAAAAGGGGAAAAATTGAGGAAAGCAGTGAATGCATTTA
                                                                                                                                                                                                                                                                                                                                                  ATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAGAAGTAAGCATTTTTCCTGTGGAAG
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                                 DB 4; Length 1050;
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                           Query Match 33.0%; Score 766; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 766; Conservative 0; Mismatches
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BX459083.2 GI:47064816
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I (Basea 1 to 160.)

I (Basea 1 to 160.)

National Institutes of Health, Mammalian Gene Collection (MGC)

Ontact: Robert Strausberg, Ph.D.

Email: capabs-r@mill.nih.gov,

Tissue Procurement: ArCC/CcTD/Drp

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be fruit; // image. Lin. gov

Plate: Library Library Arrayes

High quality sequence stop: 649.

Location/Qualifiers

// I. 1050

// Organism="Homo sapiens"

// Lissue_type="melanotic melanoma"

// Clone = "MAGE: 528993"

// Note="Organ: Skin; Vector: pCMV-SPORT6; Site_I: NotI;

Site_I: Site_I: Sall; Cloned unidirectionally. Primer: Oligo dT.

Fechnologies."
TCACGCTGTGGCAGCAAGAAGAAATGAAAATGCCTGCAAAGGAGCTCCTAAAACCT 1953
                                                                                                                                                                                                                                   1883 TCACGCTGTGGCAGCAAGGAAGAAGAATGAAAATGCCTGCAAAGGAGCTCCTAAAAACCT 1942
                                                                                                                                                                                                                                                                                                    2003 CCATCATGCACCCCGGGACTCACGTGTGGCCGCACACAGGCCCACAAACTGCAGGCTCC 2062
                                                                                                                                                                                                                                                                               GTACCTTACTAGAAAAGTTCCCCGAGACAACAGGATGCAGAAGAGGACAGATCAAATATT 2013
                                                                                                                                                                                                                                                                                                                                                       CCATCATGCACCCCGGGACTCACGTGTGGCCGCACACAGGCCCCACAAACTGCAGGCTCC 2073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 2063 GAATGCACCTGGGCTTGGTGATTCCCAAGAAGGCTGCAAGATTGGATGTGCCAAGGGA 2122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1050 bp mRNA linear EST 05-MAR-2002 5543030 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5548943
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                                                                                    1763 AGTCTTTAGAAAGAAACTGGAAGTTAATCCGAGATGAAGGCCTTGCAGTGATGAAAAG
                                                                                                                              1834 CCAAAGGTCTTTCTTGCTGAGGATGAAAACCTGAGGGAAAAAGGGGGACTGGAGCCAGT
                                                                                                                                                     BM806632.1 GI:19123455
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Homo sapiens
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5', mRNA sequence.
BM806632
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/note="Organ: Stomach; Vector: pTz18RP1; Site_1: EcoRI;
Site_2: Not1; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
iste by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The cDNA vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coll DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
competent cells E. coll ToplOF' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                          BM790814 (689 bp mRNA linear EST 05-MAR-2002 K-EST0070696 S21SNU520 Homo sapiens cDNA clone S21SNU520-16-C08 5', mRNA sequence.
BM790814 (G1:19139046
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Ramalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 689)
Kim, N.S., Hahn, Y., Oh.J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
                         882 TCACAGGTAATTGTAGAAGAAGTAAGCATTTTTCCTGTGGAAGAACAGCAGGAAGTACCA
762 GATACAGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAA
                                                                                       822 AATGAAGGGATAGAAATCACAGAAGTAACTGCTCCCCTGAGGATAATCCTGTAGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Far: +82-2860-44409
Fax: +82-42-8660-4409
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Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="S21SNU520-16-C08"
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: yongsung@mail.kribb.re.kr
Plate: 16 row: C column: 08
High quality sequence stop: 689.
Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="CSODEOLYBEL3"
//tissue type="PLACENTA"
//tissue type="PLACENTA"
//clone lib="Homo sapiens PLACENTA"
//note="Vector: PCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI-oligo(dT) primer. Five prime end enriched,
the Not I and ECRY sites of the pCMVSPORT 6 vector.
Library was not normalized."
              Unpublished (2001)
On May 22, 2003 this sequence version replaced gi:31027087.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-loigo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                           division of Invitrogen.
This sequence belongs to sequence cluster 4537.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODE012CA07QP1&c=4537.r.
Location/Qualifiers
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31.6%; Score 734; I
Best Local Similarity 99.9%; Pred. No. 0;
Matches 784; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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/db_xref="taxon:9606"
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us-09-436-184-3.oligo.rst

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/organism="Homo sapiens"

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/mol_type="mcNA"

/mol_type="mcNA"

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/lob_host="Did (Life Technologies)"

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/clone=lib="NCI CGAP EDI is a normalized CDNA library

/clone=lib="NCI CGAP EDI is a normalized CDNA library

/clone=lib="NCI CGAP EDI is a normalized CDNA library

/clone="Organ: Left Public Bone; Vector: pT713-Pac

//kharmacial with a modified polylimker; Site: is corR i;

Site_2: Not I: NCI CGAP EDI is a normalized CDNA library

/containing the following tissue(s): Chondrosarcoma cell

line CSS: The library was constructed according to

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

logor Trime CSS: The library was primed with Not

oligo-dT prime containing a Not I site. Double stranded

cDNA was ligated to an ECOR I adaptor, digested with Not

oligo-dloned directionally into pT73-Pac vector. The

oligomucleotide used to prime the synthesis of

first-strand cDNA contains a library tag sequence that is

located between the Not I site and the (dT)18 tail. The

sequence tag for this library is GCTCAAGGCT.

TAG_IEBUI-H-EDI

TAG_IEBUI-H-EDI

TAG_IEBUI-H-EDI

TAG_IEBUI-H-EDI

TAG_IEBUI-H-EDI
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National Cancer Institute / NIH
Bldg. 31 Rml0AnO Betheada, MD 20892
Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
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                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                  1 AGACCTACCAAGAGGGGGCAGCCTACCTGATGTCCCTGCAGACCTGCTGAAGCTGAGTT
                                                                                         1219 AGACCTACCAAGAGGTGGCCAGCCTACCTGATGTCCCTGCAGACCTGCAGAGCTGAAGTT
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Inpublished (1997)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
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/note="oligo dT_primed, full-length enriched cDNA library
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                                          361 CAGCAGTCCCGCCAGAAGAGGCTGAGCCACACTGAGCCCGAGGAGCAGGTTCCTGTGG
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17000532543418 GRN_ES Homo sapiens CDNA 5', mRNA sequence.
CN258120
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230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 729 Std Brror: 0.00.
Location/Qualifiers
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/mol_type="mRNA"
/dolone="IMAGE:6147375"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/lab_host=="DH108 (phage-resistant)"
/clone_lib="NIH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Insert size 2 kb. Library constructed by Life
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Fig. MRNA sequence.
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11 HAGC http://mgc.ncd.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbe.remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
http://image.llhl.gov
Plate: LiAM13477 row: b column: 16
High quality sequence stop: 634.
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GAGCTTGGGCACAGAGAGGACACTTTGCATCTGTCTGGCAACGCTCACTCTACAATGTG
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                                                                                  AATGGACTGAAAGCACAGCCTTGGTGGACCCCAAAAGAAACGGGCTACACAGAGTTAGTA
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AGENCOURT 7953975 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6010847

S, man Fequence.

BU175716

BU175716.1 GI:22689700
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1 (bases 1 to 868)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
                                                                       GCTCACTCTACAATGTGAATGGACTGAAAGCACACGCTTGGTGGACCCCCAAAAGAAACGG
                                                                                  GCTACACAGAGTTAGTAAAGTCTTTAGAAAGAAACTGGAAGTTAATCCGAGATGAAGGCC
                                                                                                                        63 GCTACACACAGAGTTAGTAAGACAGTCTTTAGAAAGAAACTGGAAGTTAATCCGAGATGAAGGCC
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                                      Length 729;
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                                    Score 578; DB 7; I
Pred. No. 1.2e-298;
0; Mismatches 1;
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                                  24.9%;
Local Similarity 99.8%;
les 628; Conservative
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481 GACTCCTTTGAGCAGGGGTATGGCAGGATGCCTCATCTTTCCGGCTGATATTCATCGTG
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.lln.gov tolumn: 24 Flate: LLAM13199 row: i column: 24 Flate: LLAM13199 row: i column: 24 Location/Quality sequence stop: 547.
                                                                                                                                                                                                                                                                                                                                                                                            Length 868;
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Pred. No. 4.4e-298;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                         tch 24.8%;
al Similarity 99.8%;
627; Conservative 0
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583 bp mRNA linear EST 17-SEP-2004 BP364957 Sugano cDNA library, fetal lung fibroblast TIG Homo sapiens cDNA clone TIR05529, mRNA sequence. BP364957 BP364957.1 GI:52295202
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Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Concact: Yuteka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 583)
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/clone_lib="Sugano cDNA library, fetal lung fibroblast
TIG"
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100.0%; Pred. No. 1.4e-29
tive 0; Mismatches 0
1341 CAGAGATTAGTTCAACTATTTCCCAATG 1368
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/organism="Homo sapiens"
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/cell_type="fibroblast"
/cell_line="TIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TIR05529"
                 576 CAGAGATTAGTTCAACTATTTCCCAATG
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 603)
S Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
L Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
He-1, Shirokanedai, Minacku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
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                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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/clone="SMR06083"
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/cell_type="smooth muscle cell"
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100.0%; Pred. No. 2.9e-293;
:ive 0; Mismatches 0;
                                                                              BP336604.1 GI:52266184
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OY 1522 TTGCTGAGAGCATCCCATATTTAAAGGAAGGAATAGAATCCGGAGATCCTGGCACTGATG 1581	Yammanoto, J., Wakamateu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T. Isogai, T. JOHAL Unpublished (2000) COMMENT Contract: Takeo leogai Genonics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel 81-438-52-3986 Email: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute of Medical Science, University of Tokyo, and Halix Research Institute of Medical Science, University of Tokyo, and Helix Research Institute of Medical Science, University of Tokyo, and Helix Research Institute of Medical Science, University of Tokyo, and Helix Research Institute and Science, University of Tokyo, and Coganisms—"Homo sapiens" Ab Zref="raxon:9606" (Clone="raxon:9606" (Clone="raxon:	ORIGIN Query Match Acthoric acid (RA) induction Beet Local Similarity 99.7%; Pred. No. 8.8e-287; Indels 0; Gaps 0; Matches 656; Conservative 0; Mismatches 2; Indels 0; Gaps 0; QY 1013 AAATAATTGATAAGACTATTAAAGCTGAACAAAAACTCCGTAAAG 1072

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/tissue type="PLACENTA"
/tissue type="PLACENTA"
/tissue type="PLACENTA"
/clone lib="Homo saptens PLACENTA"
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May 13, 2003 this sequence version replaced gi:30635043.
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                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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                                         /dev_stage="Adult"
/clone_lib="BN0047"
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/note="Corgan: breast_normal; Vector: puc18; Site_l: Smal;
/note="Corgan: breast_normal"
Site_l: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Li, Wass, I to 1011)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length, CDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261
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Pred. No. 8.3e-280;
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                        xref="taxon:9606"
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100.0%; Pred
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                                                                                                                                                                                                         CTGATGATGGGAGATTTTATTTCCACCTGGGGATGCCATGCAGAGGGTTGGGAACAAAG 1635
                                                                                                                                                                                                                                                         BP266690 Sugano cDNA library, thyroid JTH Homo sapiens cDNA clone BP266690
                                                                                                                                                                  1158 CAGTGTGAGGATGATTTGGCTGAGAAGAGGAAGTAATGAGGTGCTACGTGGAGCCATC 1217
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                              292 GIGTGACACCTAATGATGGCTTTGCTAAAGTCCATTATGGCTTCATCCTGAAGCACAGA
                                             GTGTGACACCTAATGATGGCTTTGCTAAAGTCCATTATGGCTTCATCCTGAAGGCACAGA
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/db Xzef="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone l1b="eRN EB"
/note="oligo dr primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hBS cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
                                                                                                                                           769
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                                                                                                            TCGAGACCTACCAAGAGGTGGCCAGCCTACCTGATGTCCCTGCAGACCTGCTGAAGCTGA 1275
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1 (Dases 1 to 589)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L.W.

Transcriptome characterization elucidates signaling networks that Nat. Biotechnol. 22 (6), 707-716 (2004)

Regenerative Medicine
CAGTITICACAAGACTGTAATCAGGATATGGAAGAGATGATGTCTGAGCAGGAAAATCCAG
                                                          770 CAGTTTCACAAGACTGTTATCAGGATATGGAAGAGATGATGTCTGAGCAGGAAAATCCAG
                                                                                        Gaps
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Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 589 Std Error: 0.00.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   CN258117
CN258117.1 GI:47274531
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Homo sapiens numeary.

Homo sapiens by Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

CE | (bases 1 to 765)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Office of Cancer Genomics

Notional Cancer Institute / NIH

Bldg. 31 Rml0AO7 Berbesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue procurement: Irene Ginis and Mahendra Rao, NIA

CDNA Library Preparation: Yulan Piao and Minoru Ko

CDNA Library Preparation: Yulan Piao and Minoru Ko

CDNA Library Preparation: Yulan Piao and Minoru Ko

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC c

can be found through the I.M.A.G.E. Consortium/LINL at:

http://mage-llnl.gov

Plate: NDAM511 row: a column: 24

High quality sequence stop: 605.

Location/Qualifiers

Location/Qualifiers
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AGENCOURT_14550808 NIA Human H1 Embryonic Stem Cell cDNA Library
(Long) Homo sapiens cDNA clone IMAGE:30425975 5', mRNA sequence.
CD643948
                                                                                                                                                                                                                                                                                                                                                                                                                                     2131 AGACCAGGACCTGGGAGGAAGGCAAGGTGCTCATCTTTGATGACTCCTTTGAGCACGAGG
                                                                                                                                                                                                                     CCTGTACCTTACTAGAAAAGTTCCCCGAGACAACAGGATGCAGAAGAGGACAGATCAAAT
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AAGCCAAAAGGTCTTCCTGCCTGAGGATGAAAACCTGAGGGAAAAAGGGGAACTGGAGCC
                                                                                                                                                                                                    AGTICACGCTGTGCCAGCAAGGAAGAAGAATGAAATGCCTGCAAAGGAGCTCCTAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30425975"
/tissue_type="Embryonic Stem cells"
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                                                                                                                         1397
                                                                                                                                                                                             GTGACACCTAATGATGGCTTTGCTAAAGTCCATTATGGCTTCATCCTGAAGGCACAGAAC 1517
                                                                                                                                                                                                                                                                                                                                     1518 AAAATTGCTGAGAGCATCCCATATTTAAAGGAAGGAATAGAATCCGGAGATCCTGGCACT 1577
                                                                                                                                                                                                                                                                                                                                                                                                          1578 GATGATGGGAGATTTTATTTCCACCTGGGGATGCCATGCAGGGTTGGGAACAAGAG 1637
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Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@imm.u-tokyo.ac.jp.
                                                                                                                                                                                                                                344
                                                                                                                                                                                                                                                                                            GAGACCTACCAAGAGGTGGCCAGCCTACCTGATGTCCCTGCAGACCTGAAGCTGAGT 164
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 582)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGAGCTTGGGCACAAGAGAGACACTTTGCATCTGTCTGGCAACGCTCACTCTACAATG
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                                                                                      Troaagcorcocrcagacaacaacaarrrcraggrcarargagaggrrccragrracc
                                                                                                                       CTGCAGAGATTAGTTCCAACTATTTCCCAATGATACTTCCTTAAAAAATGACCTTGGCGTG
                                                                                                                                            225 CTGCAGAGATTAGTTCAACTATTCCCAATGATACTTCCTTAAAAAATGACCTTGGCGTG
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/clone="KAR01529"
/tiseuc_type="small intestine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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Homo sapiens
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BP270196
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Contact: MIPS
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                         /cell_line="WA01"
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                                                                                                                                                                                                                                                                                                               GGAGCAGGTTCCTGTGGAGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAAT 463
                                                                                                                                                                                                                                                                                                                                            TCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACA 523
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TTACCACGTGGAAGACAGTTTCACAAGACTGTAATCAGGATATGGAAGAGATGTC 703
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579; Conserva
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Best Local S:
Matches 579,
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517 bp mRNA linear EST 04-SEP-2003
DKFZp686L22209_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686L22209_5', mRNA sequence.
BX479249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (Dasses 1 to 517)
Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.
EST (Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., et al.)
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from 5. Wiemann, Molecular Genome Analysis German Cancer
Research Center (DKFZ); Email 8. Wiemann@dkfz- heidelberg.de;
Research Center (DKFZ); Email 8. Wiemann@dkfz- heidelberg.de;
Requenced by GBF (National Research Center for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp686122209) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcentent, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANN; Email: clone@rzpd.de.
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                              1046 TGATGCTGCAGAAAAACTCCGTAAAAGGGGAAAAATTGAGGAAGCAGTGAATGCATTTAA 1105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 517)
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/note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
ACAGGTAATTGTAGAAGTAAGCATTTTTCCTGTGGAAGAACAGCAGGAAGTACCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            926 ACAGCAGGAAGTACCACCAGAAACAAATAGAAAAACAGATGATCCAGAACAAAAAGCAAA
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                                                                                                            944 AGAAACAAATAGAAAAACAGATGATCCCAGAACAAAAGCA 983
                                                                                                                                              Query Match 22.2%; Score 517; DB 5; Le Best Local Similarity 100.0%; Pred. No. 7.8e-266; Matches 517; Conservative 0; Mismatches 0;
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Homo sapiens (human)

SM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 711)

Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,

Li,Y., Xu,C., Fang,R., Guegler,R., Rao,M.S., Mandalam,R.,

Lebkowski,J and Stanton,L.W.

Transcriptome characterization elucidates signaling networks that

control human ES cell growth and differentiation

Nat. Blotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R

Regenerative Medicine

Geron Corporation
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/mol type="mRNN"
/mol type="mRNN"
/mol type="mRNN"
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derived from H1, H7 and H9 cells"
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/note="oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 16-MAY-2004
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                                                                                      241 ITCTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAG
                                                                                                                                                                                                            353 TTGTTGACTATGAGGAAGTTCTAGGAAACTAGGAATCTATGATGCTGATGGTGATGAGGA
                                                                                                                                                                                                                                                       ATTITGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAAAGAGAGATCTACTTCAGAGC
                                                                                                                                                                                                                                                                                 421 AGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG
        233 AGCATGGAGGACACAAGAATGGGAGGAAGGAAGGCGGACTCTCAGGAACTTCATTCTTCACGT
                                                                                                                                                                                                                                                                                                                                         CAGCAGTCCCGCCAGAAGAGGCTGAGCCACACTGAGCCCCGAGGAGCAGGTTCCTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CN368832 711 bp mRNA linear EST 16
17000418219954 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 711 Std Error: 0.00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 558
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CN368832.1 GI:47368766
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(Dasse; 1 to 721)

(S NIH-MGC http://mgc.nci.nih.gov/.

Insulished (1999)

Lontact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue procurement: AfrCC

cDNA Library Preparation: Life Technologies, Inc.

CLONA Library Preparation: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Locality sequence stop: 719.

High quality sequence stop: 719.

Localin/Qualifiers
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/organism="Homo sapiens"
/mol type="mRNA"
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/clone="ymAdE:51138622"
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/clone lib="NIH MGC_12"
/note="Togan: cervix, Vector: pCMV-SPORT6; Site_1: Not1;
/not1;
/rechnologies insert size 1.4 kb. Library prepared by Life
Technologies."
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602996326F1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:5138622 5',
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                                                                                                                                             TCGCTCAGACAGCAACAATTTCTAGGTCATATGAGAGGTTCCCTGCTTACCCTGCAGAG 1345
                                                                                                                                                                                                                             1346 ATTAGTICAACTATTTCCCCAATGATACTTCCTTAAAAAATGACCTTGGCGTGGGATACCT 1405
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                                                                                    421 ATTAGTTCAACTATTTCCCAATGATACTTCCTTAAAAAATGACCTTGGCGTGGGATACCT
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                                                                                                                                                                                                                                                                                                                  1406 CTTGATAGGAGATAATGACAATGCAAAGAAGTTTAT 1442
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Homo sapiens
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Best Local Similarity 99.8
Matches 557; Conservative
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:960"
/db_xref="taxon:960"
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/tissue_type="large cell carcinoma"
/lab_most="DH10B (phage=resistant)"
/clone_lib="WHH MGC 68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       636 GAGCATAGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGAAAGAG 695
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Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                 GAACAAATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGAC
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                                                                                                                                                                                                                                                                                                                                                 Length 868;
                                                                                                                                                                                                                                                                                                                                         tch 21.1%; Score 491; DB 5; Length 86 al Similarity 100.0%; Pred. No. 8.4e-252; 491; Conservative 0; Mismatches 0; Indels
  Location/Qualifiers
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                                                                                                                                                     227
                                                                                                                                                                                      GGTTTANGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 AAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCCACAG
                                                             Gaps
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0
               Length 711;
                                                        1; Indels
            Score 493; DB 7; I
Pred. No. 6.8e-253;
0; Mismatches 1;
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       Query Match
Best Local Similarity 99.8%;
Matches 543; Conservative
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602692270F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4824712 5', mRNA sequence.
                                                                                                                                                                                                                                                          /tissue_type="embryonic stem cells, cell lines H1, H7, and H9"
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/note="doligo dT primed, full-length enriched cDNA library
/note="condifferentiated hES cell lines H1 (p32), H7 (p29),
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"
          networks that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAA
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      Transcriptome characterization elucidates signaling control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                         Length 770;
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                                                                               Regenerative Medicine
Geron Corporation
730 Constitution Drive, Menlo Park, CA 94025, U
781 650 473 8658
Fax: 650 473 7760
Email: rbrandenbergeregeron.com
Insert Length: 770 Std Error: 0.00.
                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                             organism="Homo sapiens"
                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
 Lebkowski, J and Stanton, L.W
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Best Local Similarity 99.8%;
Matches 511; Conservative
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                                                                                                                                                                                                                                                                /clone_lib="GRN_PREHEP"
/note="oligo dT_primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"
                                                                                                                                                                                                                                                                                                                                                                                                                                   490
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Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99
                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/tisaue_type="embryonic stem cells, DMSO-treated H9 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                611 ACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGACAGTTTCACA
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328775548 GRN_ES Homo sapiens CDNA 5', mRNA sequence.
CN368823
                                                                                                                                                                                                                                                                                                                                                                   Length 520,
                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, 1
281 ESS 0473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
                                                                                                                                                                                                                                                                                                                                                                     20.5%; Score 476; DB 7; Le
100.0%; Pred. No. 9.1e-244;
ive 0; Mismatches 0;
                                                                                                                                           0.00
                                                                                                                                                                                         organism="Homo sapiens"
                                                                                                                           Email: rbrandenberger@geron.com
Insert Length: 520 Std Error:
    Location/Qualifiers
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Homo sapiens
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476; Conservative
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Best Local S:
Matches 476,
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Bukaryota, Wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Wetazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 455)

S Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,

Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,

Lebkowski, J and Stanton, L. W.

Transcriptome characterization elucidates signaling networks that

control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R

Regenerative Medicine

Geron Corporation

Geron Corporation

John Shands Shands
                                                                                                                                                                                                                                                                                                          CN274513 455 bp mRNA linear EST 16-MAY-2004 17000600026439 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
                                1179 GAGAAGAGGAGAAGTAATGAGGTGCTACGTGGAGCCATCGAGACCTACCAAGAGGTGGCC 1238
421 AGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1239 AGCCTACCTGATGTCCCTGCAGACCTGCAGAGTTTGAAGCGTCGCTCAGACAGG 1298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1359 TTTCCCAATGATACTTCCTTAAAAATGACCTTGGCGTGGGATACCTCTTGATAGGAGAT 1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="GRN_PREHEP"
/note="oligo dT_primed, full-length enriched cDNA library
from DNSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRND,8"
/db_xref="texon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1059 AAACTCCGTAAAAGGGGAAAAATTGAGGAAGCAGTGAATGCATTTAAAGAACTAGTACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1119 AAATACCCTCAGAGTCCACGAGCAAGATATGGGAAGGCGCAGTGTGAGGATGATTTGGCT
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19.6%; Score 455; DB 7; Le
Best Local Similarity 100.0%; Pred. No. 1.8e-232;
Matches 455; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: rbrandenberger@geron.com
Insert Lenghr: 455 Std Error: 0.00.
Location/Qualifiers
1. 455
                                                                                                           481 AAATGGTACACGCAGAACATGTTGAGGGA 509
                                                                                                                                              CN274513
CN274513.1 GI:47290927
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                                                                                                                                                                                                                                                   RESULT 25
CN274513
LOCUS
DEFINITION
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KEYWORDS
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                             Busaryotes, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bataryotes; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

MINHMGC Hup://mgc.ndi.nih.gov/.

MINHMGC Hup://mgc.ndi.nih.gov/.

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue procurement: Miklos Palkovits, M.D., Ph.D.

Contact: Robert Strausberg, Ph.D.

Tissue procurement: Miklos Palkovits, M.D., Ph.D.

CONA Library Arrayed by: The I.M.A.G.B. Consortium (LLML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be through the I.M.A.G.B. Consortium/LIML at:

Consortium/LIML at:

Flate: LLAMU036 row: k column: 17

High quality sequence stop: 685.

Location/Qualifiers

I. . 689

/ Arrayer-mana,

// Ab nose="Minds" Resis; Vector: pBluescriptR (modified pluescript KS+); Site=1: BanHi; Site=2: Sall-XhoI

// Alb hose="Minds" Site=1: BanHi; Site=2: Sall-XhoI

// Alb hose="Minds" Site=1: BanHi; Site=2: Sall-XhoI

// Site=1: LLAMUNG Colf primed using primer

// Alb hose="Minds" Site=1: BanHi; Site=2: Sall-XhoI

// Site=3: BanHi; Site=3: Sall-XhoI

// Site=3: BanHi; Site=3: Sall-XhoI

// Site=3: BanHi; Site=3: Sall-XhoI

// Site=3: Sall-XhoI
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19.7%; Score 458; DB 4; Length 689;
Best Local Similarity 99.8%; Pred. No. 4.6e-234;
Matches 508; Conservative 0; Mismatches 1; Indels
            sapiens (human)
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Gaps .; 0 9

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/ussue_type="dorsal root ganglia"
/dev stage="adult, 36 yr"
/dev stage="adult, 36 yr"
/lab_host="DH10B"
/lab_host="DH10B"
/clone_lib="Lupski_dorsal root ganglion"
/clone_lib="Lupski_dorsal root ganglion"
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/note="Vector: pCWV-SPORT6" (Life Technologies); Site_1:
/note="Vector: pCWV-SPORT6" (Life Technologies); Site_1:
/note="Vector: pcmv-sport" (Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
// mockets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Ta (bases 1 to 857)

NH-MGC http://mgc.nci.nih.gov/.

RS NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL (Dapublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbar remail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

http://image.llnl.gov

plate: LibMa13565 row: n column: 04

High quality sequence stop: 590.
                                                                                                                                                                                                                                                                                                                                                               BQ889709
AGENCOURT 8118183 Lupski dorsal root ganglion Homo sapiens CDNA clone IMAGE:6181443 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCAGCGGCAACAGCAGCAGCGGCG
                           375 CACAGCCTTGGTGGACCCCCAAAGAAAGAAAGGGGCTACACAGAGTTAGTATAGTCTTTAGAAA
                                                                                                  1846 TCCTGCCTGAGGATGAAAACCTGAGGGAAAAAGGGGACTGGAGCCAGTTCACGCTGTGGC
                                                                                                                                                                                            495 TCCTGCCTGAGGATGAAAACCTGAGGGAAAAAGGGGGACTGGAGCCAGTTCACGCTGTGGC
1726 CACAGCCTTGGTGGACCCCAAAAGAAACGGGCTACACAGAGTTAGTAAAGTCTTTAGAAA
                                                                           1786 GAAACTGGAAGTTAATCCGAGATGAAGGCCTTGCAGTGATGGATAAAGCCAAAGGTCTCT
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19.4%; Score 450; DB 5; Length 857;
Best Local Similarity 99.8%; Pred. No. 9.8e-230;
Matches 500; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6181443"
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                                                                                                                                                                                                                                                                                    555 AGCAAGGAAGA 568
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BQ889709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1606 GGGATGCCATGCAGGGTTGGGAACAAAGAGGCATATAAGTGGTATGAGCTTGGGCACA 1665
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1. bases 1 to 583)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1486 TCCATTATGGCTTCATCCTGAAGGCACAGAACAAAATTGCTGAGAGCATCCCATATTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 ATGATACTTCCTTAAAAATGACCTTGGCGTGGGATACCTCTTGATAGGAGATAATGACA
        Gaps
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Pred. No. 7.68-231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="RCT00312"
/tissue type="rectum"
/clone_lib="Sugano cDNA library, rectum"
                                                                                                                                                      GCTAAAGTCCATTATGGCTTCATCCTGAAGGCACA 1513
                                                                                                                                                                         19.4%; Score 452; DB
ilarity 99.6%; Pred. No. 7.6e
Conservative 0; Mismatches
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/organism="Homo sapiens"
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/db xref="taxon:9606"
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Homo sapiens
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BO722578 11near EST 16-JUL-2002
AGENCOURT 8215289 Lupski_sympathetic_trunk Homo sapiens CDNA clone
IMAGE:618766 5', mRNA sequence.
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    217
                                                                           337
                                                                                                    338 GGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC 397
                                                                                                                            TTGTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAG 300
                                                                                                                                                                ATITICATGIGGAIGAIGCCAAAGTITIATIAGGACTIAAAGAGAGAICTACTICAGAGC 360
                                                                                                                                                                                                   CAGCACTCCCGCCAGAAGAGGCTGAGCCACACACTGAGCCCGAGGAGCAGGTTCCTGTGG 420
                                                                                                                                                                                                                                      CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCA
                 GGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Lupski_sympathetic_trunk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                     AAATGGTACACGCAGAACATG 501
                                                                                                                                                                                                                                                                                                                                                                     BQ722578
BQ722578.1 GI:21861475
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Homo sapiens
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BQ722578
LOCUS
DEFINITION
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KEYWORDS
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ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
Not1; Site_2: Sal1; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGGGTCCG-3' and
5'-ATCATAGTTCTAGATCGGACGGCCCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor Technologies); available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTCCGGCAGCGGTAGCACGAGTGCGGGCAGCAGCAGCCCCGGGGCCCGGAGAGACAA 120
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Homo sapiens
Homodata; Craniata; Vertebrata; Buteleoston
Homamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Homodattp://mgc.nci.nih.gov/.
Nutl-MGC http://mgc.nci.nih.gov/.
Nutl-MGC http://mgc.nci.nih.gov/.
Homodat: Robert Strausberg, Ph.D.
Email: cgapbs r@mal.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                          Length 920;
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Pred. No. 9.9e-230;
0; Mismatches 1; Indels
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BU190749 GI:22704733
EST.
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Best Local Similarity 99.8%;
Matches 500; Conservative 0
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/organism="Homo sapiens"
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Matches 548; Conservative
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 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can life and through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov i column: 04
High quality sequence stop: 695.
Location/Qualifiers
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                                                                                                                           HRI human cDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuho,Y., Isogai,T.)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 767)
                                                                                                                                                                                                                    Contact: Take 1 segai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-396
Email: genomics@hri.co.jp
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
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                                                                Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J. Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuho,Y. and
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/organism="Homo sapiens"
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(Dases I to 519)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Burnstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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QV2-NN0045-181200-560-d11 NN0045 Homo sapiens CDNA, mRNA sequence.
BF962729
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Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Final: saingson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-181200-560-401at3=2000-12-18t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 518.
CAGAAGTAACTGCTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG 900
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                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/mol_type="matNA"
/db xref="taxon:9606"
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/clone lib="WIH MGC bibrary constructed by ling Hong in the laboratory of Gerald M. Rubin (University of Callfornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Supersoribt II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                     AGENCOURT_10023130 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6480917 BU502606
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/PTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLCR2661 row: h column: 06
High quality sequence stop: 678.
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1 (bases 1 to 911)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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19.2%; Score 447; DB 5; Length 911;
Best Local Similarity 100.0%; Pred. No. 4.1e-228;
Matches 447; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BU502606.1 GI:22807596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
Homo sapiens
                                                                                                                                       541 GAGAACCACA 550
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COMMENT
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BU502606
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452 418 512 358 572 298 632

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/mol_type="mRNA"
//mol_type="mRNA"
/dob_xref="taxon:9606"
/dob_stage="Adult"
/clone lib="Nd0045"
/note="Organ: nervous normal; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - ludwig Institute for Cancer Research)
No. 196,716 - ludwig Institute for Cancer Research)
tissue mRNA and CDNA amplification were performed under
low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNSBBB27 695 bp mRNA linear EST 16-MAY-2004
17000424344521 GRN_EB Homo sapiens CDNA 5', mRNA sequence.
CN368827
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 695)
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Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.
                                                                                                                                                                                                                                                                                                      Length 537;
                                                                                                                                                                                                                                                                                                  18.8%; Score 436; DB 2; Length 53 99.8%; Pred. No. 3.1e-222; ive 0; Mismatches 1; Indels
High quality sequence stop: 533. 
Location/Qualifiers 1. 537 / /organism="Homo_sapiens"
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Homo sapiens
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Matches 486; Conservative
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AUTHORS
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                      PEATURES
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mail: asimpson@ludwig.org.br
This sequence was derived from the FAPBSP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
futp://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV2-NN0045-220
800-323-f03&t3=2000-08-22&t4=1)
Seq primer: puc 18 forward
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Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Eukaryota, Merazoa, Chordates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 537)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
G.Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
G.Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE935834 SY 02-OCT-2000 OV-2-NN0045-220800-323-£03 NN0045 Homo sapiens CDNA, mRNA sequence.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                     GAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCACAGGAGAACCACAA
                                                                                                                                                                                                                                                GAGGATGATGAGTTTCTTATGGCGACTGATGTAGATGATAGATTTGAGACCCTGGAACCT
                                                                                                                                                                                                                                                                                                                   GAAGAGGCTGAGCCACACACTGAGCCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACCCCAG
                                                                                                                                                  AATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATGAAATGGTACACGCA
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proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
       Length 519;
                                           Indels
         18.8%; Score 438; DB 4; L6
100.0%; Pred. No. 2.5e-223;
ive 0; Mismatches 0;
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             Query Match 18.8
Best Local Similarity 100.
Matches 438; Conservative
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Euteleostomi;

Fisk, G.J.,

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                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. (bases 1 to 554)
Poustka, A., Wellenreuther, R., Mewes, H.W., Weil, B. and Wiemann, S.). EST (Poustka, A., Wellenreuther, R., Mewes, H.W., Weil, B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300
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                                                                                                                                                                                                                                                                                                     Tingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZDSEKOLI18) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerveg 6, 14059
Berlin-Charlottenburg, GERMANN; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ATCCGGAGATCCTGGCACTGATGATGATGGGAGATTTTATTTCCACCTGGGGGATGCCATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GAGGGTTGGGAACAAAGAGGCATATAAGTGGTATGAGCTTGGGGCACAAGAGAGGACCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1559 ATCCGGAGATCCTGGCACTGATGATGGGAGATTTTATTTCCACCTGGGGGATGCCATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1679 IGCAICTGTCTGGCAACGCTCACTCTACAATGTGAATGGACTGAAAGCACAGCCTTGGTG
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99.8%; Pred. No. 2.6e-216;
tive 0; Mismatches 1;
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Best Local Similarity 99.84
Matches 475; Conservative
                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                           Contact: MIPS
MIPS
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                                                                                                                                                                                                                                                                                    1. .695

/ organism="Homo sapiens"
//mol_type="manNa"
//db xref="taxon:9606"
/ tissue type="embryonic stem cells, embryoid bodies
/ tissue type="embryonic stem cells"
/ clone lib="GRN EB"
/ note="oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
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AL700393 GI:19620926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcriptome characterization elucidates signaling networks that control human BS cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R

Regenerative Medicine
Geron Corporation

Fast. 650 473 8658

Fax: 650 473 760

Email: rbrandenbergerencom.com

Insert Length: 695 Std Error: 0.00.
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18.5%; Score 430; DB 7; I
Best Local Similarity 99.8%; Pred. No. 5.4e-219;
Matches 480; Conservative 0; Mismatches 1;
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us-09-436-184-3.oligo.rst

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Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s. wiemann@dkfz- heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424 bp mRNA linear EST 04-SEP-2003 DKFZD762H093 r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZD762H093-5', mRNA sequence.
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                                                                                                                                                                                                                                                                                             Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 424)
1 (bases 1, K.) Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Koehrer, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No sl sequence available.

No sl sequence available.

This clone (DKEZp762H033) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers
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                                                                                                                                                                             481 AAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCACAG
                                                                                                                                                                                                         CAGCAGTCCCCCCCACAAGAAGCCTGAGCCACACTGAGCCCCGAGGAGCAGGTTCCTGTGG
                                       400 cháchártccaccháhánaháchtanacchacharanachanachadanacharachara
                                                                                        AGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG
                                                                                                                              460 AGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG
                                                                                                                                                                                                                                                                   541 GAGAACCACAACAAGAAGATGATGAGTTTCTTATGGCGACTGATGTAGATGATTTG
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/dev_stage="bH10B"
/clone lil=="762" (synonym: hmel2)"
/clone lil=="762" (synonym: hmel2)"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sall"
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18.2%; Score 424; DB 1; Length 424;
Best Local Similarity 100.0%; Pred. No. 8.4e-216;
Matches 424; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                               601 AGACCCTGGAACCTGAAGTATCTCATGAA 629
                                                                                                                                                                                                                                                                                                                                                                                                         640 AGACCCTGGAACCTGAAGTATCTCATGAA 668
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/db_xref="taxon:9606"
/clone="DKFZp762H093"
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/db_xref="taxon:9606"
/clone="INABA"
/lab_nost="anabas:6480842"
/tlasue type="carcinoma, cell line"
/clone libe-"NUH MGC_40"
/clone libe-"NUH MGC_40"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIX/NoI sites using the
following 5' adaptor: GGGACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit-
(Stratagene) and Superscript II T (Life Technologies).
Note: this is a NIH_MGC Library."
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                              959 bp mRNA linear EST 12-SEP-2002 10023079 NIH_MGC_40 Homo sapiens CDNA clone IMAGE:6480842
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NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Upublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Proturement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLOM2661 row: e column: 03
High quality sequence stop: 591.
                                                                                                                                                                                                                  Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 GGTTTATGGTGATTGCATTGCTGGGCGTCTGAACATCTGTAGCTGTCGTTTGGTTTGATC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 959)
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ilarity 99.4%; Pred. No. 2.8e-216;
Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
                                                                                                                            BU502544.1 GI:22807433
                                                                                                                                                                        Homo sapiens (human)
                                                                                 5', mRNA sequence.
BUS02544
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Best Local Similarity
Matches 625; Conserv
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Bulkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bulkaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 504)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Magal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Shotgun aequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                    GCTCCGGCAGCGGTAGCACGAGTGCCGGCAGCAGCACCCCGGGGCCCGGAGAGACAA 120
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QV2-NN0045-041000-403-b08 NN0045 Homo sapiens CDNA, mRNA sequence.
BF943222.1 GI:12360497
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        carried out using a Not I primer-adapter [5.-pdcTyGATGTCTAGATCCGCGCC(T):5.3']. cDNA was cloned in Not I/Sal I sites. EST analysis was performed the NIH Intramural Sequencing Center (NISC)."
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                            CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCGGCAACAGCAGCAGCAGCAGCAGCA
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                     Length 606;
                                                                                                                                1; Indels
                                                                                               18.2%; Score 424; DB 7;
99.8%; Pred. No. 9e-216;
Live 0; Mismatches 1
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Homo sapiens
                                                                                                               Best Local Similarity 99.8
Matches 474; Conservative
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Fax: +55-11-2707001
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GAGCCACACACTGAGCCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACCCCCAGAATATCGAA
                                                           GATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTT
                                                                                                                         181 GATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTT
                                                                                                                                                                                                                         564 GAGTITCTTATGGCGACTGATGTAGATTGGAGACCCTGGAACCTGAAGTATCT
                                                                                                                                                                GAGGGAGAGACTTGCAACAAGAAGATGGACCCACAGGAGAACCACAACAAGAGGATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expires
Descriptes
Unpublished (2004)
Conteat: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/31, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graemeéhelix.nih.gov
Plate: 08 row: b column: 05
Seq primer: MJRP1 reverse primer (ABI).
Location/Qualifiers
606
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mol type="mxN."
db xref="taxon:9606"
clone="hw08b0s"
clone="hw08b0s"
dev stage="adult"
lab_host="EMDH108"
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CN481470
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human ocular

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//note="Correction" in the part of the confidence of the confidence of the corrected from primary human pericytes in culture. A directionally cloned primary human pericytes in culture. A directionally cloned cDNA library in the pSPORTI vector (Invitrogen) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5-pacTrandArdCGCAGCCCC(C(T)]5-3']. CDNA was [5-pacTrandArdCGCAGCGCCCC(T)]5-3']. CDNA was cloned in Not I/Sal I sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC)."
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Unamplified (hw)"
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                 primary
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               cultured
                                                                                  Section on Molecular Structure and Function National Eye Institute 6/331, NIH, Bethesda, MD 20892-2740, USA Fax: 301 402 3452 Pax: 301 496 0078
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18.2%; Score 423; DB 7; L
Best Local Similarity 99.8%; Pred. No. 3.1e-215;
Matches 473; Conservative 0; Mismatches 1;
                 analysis of
                                                                                                                                                                                Email: graeme@helix.nih.gov
Plate: 08 row: b column: 10
Seq primer: MI3RPI reverse primer
Location/Qualifiers
                                                                                                                                                                                                                                                                          organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                /cell_type="pericytes"
/dev_stage="Adult"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                  /clone="hw08b10"
Tsal, J.Y. and Wistow, G. Expressed sequence tag
                                        pericytes
Unpublished (2004)
Contact: Wistow G
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/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/dev_stage="Adult"
/clone lib="NN0045"
/note="Organ: nervous normal; Vector: puc18; Site_1: Smal;
/note="Organ: nervous normal; Nector: Reverse products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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             Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome roject. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-041000-403-b08&t3=2000-10-04&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 504.
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 610)
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                                                                                                                                                                                                                                                                                                                                                                                                                              Score 423; DB 4; Length 504;
Pred. No. 3e-215;
0; Mismatches 1; Indels
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/organism="Homo sapiens"
//organism="Momo sapiens"
//db zref="nRNA"
//db zref="taxon:9606"
//dev_stage="Adult"
//clone_lib="Cyr0549"
//note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning_products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puC 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, 1 (Mamalla, Eutheria, Primates; Catarrhini, Hominidae, Homo. 1 (Dases 1 to 433)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F., Goldman, G.H., Carvalho, A.F., Mateukuma, A., Baia, G.S., Simpson, D.H., Burnetein, A., Goliveira, P. S., Bucher, P., Jongeneel, C.V., Simpson, D.H., Simpson, A., Simpson, D.H., Simpson, A., San, S., Simpson, S., Simpson, S., Simpson, S., Simpson, S., Simpson, A., Si
                                                                              BQ318605 433 bp mRNA linear EST 17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
Fax: +55-11-2707001
Email: saingson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gerhtml2.pl?tl=CM0&t2=CM0-CT0549-210900-561-a04&t3=2000-09-21&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 433.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
2020263
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llarity 100.0%; Pred. No. 1.4e-212;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                  BQ318605.1 GI:20924374
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Homo sapiens
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                                                             AU138660 AU138660 PLACE1 Homo sapiens cDNA clone FLACE1009036 5', mRNA
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Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TGAACCTCTAGAAAATGAAGGGATAGAAATCACAGAAGTAACTGCTCCCCCTGAGGATAA 120
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            749 AAGATTGCACCATGATACAGATGATGTAACATACCAAGTCTATGAGGAACAAGAGTATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
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Acrganism="Homo sapiens"
mol_type="mRNA"
db_xref="taxon:9606"
/clone="PLACEI009036"
/tissue_type="placenta"
/clone_lib="placenta"
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Unpublished (2000)
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Homo sapiens
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Matches 420; Conservative
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Location/Qualifiers
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/db_xref="taxon:9606"
/dev_stage="Adult"
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                                                                                                                                                                                                 DUL/BDUS 1100 bp mRNA linear EST 07-MAY-2002
AGENCOURT_6773215 NIH_MGC_128 Homo sapiens CDNA clone IMAGE:5811567
                                                                         ATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAAAATGAAGGGATAGAAAT 838
                        AGATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCATGATACAGATGATGAAC 778
                                         GACAGITICACAAGACIGIAAICAGGAIAIGGAAGAGAIGAIGAIGTCIGAGCAGGAAAAICC 255
                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 1100)

NHF-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                         CACAGAAGTAACTGCTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTA 896
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http://image.llnl.gov
Plate: LLCM2060 row: j column: 16
High quality sequence stop: 394.

1. 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
                                                                                                                                                                                                                                                              BQ278505.1 GI:20488713
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                                                                                                                                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                              839
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AUTHORS
TITLE
JOURNAL
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Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Go'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtm12.pl?tl=QV2&t2=QV2-NN0045-181200-563-all&t3=2000-12-18&t4=1)
Seq primer: puc 18 forward
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QV2-NN0045-181200-563-a11 NN0045 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                      295 GAACAAATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGAC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               576 GCGACTGATGTAGATAGATTTGAGACCCTGGAACCTGAAGTATCTCATGAAGAAACC 635
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Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bumania; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 444)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 636 GAGCATAGCTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGAA 692
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                                                                                                                                                                                                                                              235 GAGCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACCCCCAGAATATCGAAGATGAAGAAAAA
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
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/lone lib="Human Retina cDNA (Un-normalized, unamplified): hd/he" (Un-normalized, unamplified): hd/he" (Un-normalized, normalized, normanified): hd/he" (Nordor E) (N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer-adapter
{5'-pGACTAGTTCTAGATCGCGAGCGGCCC(T)15-3']. EST analysis
was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC)."
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7000600180518 GRN_PRENEU Homo sapiens CDNA 5', mRNA sequence.
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 740)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1628 GAACAAAGAGGCATATAAGTGGTATGAGCTTGGGCACAAGAGAAGACACTTTGCATCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 CTGGCAACGCTCCACCACTACAATGTGAATGGACTGAAAGCACGCTTGGTGGACCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        462 IGCCTGCAAAGGAGCTCCTAAAACCTGTACTTACTAGAAAAGTTCCCCGAGACAACAACAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1688 CTGGCAACGCTCACTCTACAATGTGAATGGACTGAAAGCACAGCCTTGGTGGACCCCAAA
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                      Location/Qualifiers
1. .570
/organism="Homo sapiens"
                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="he17b04"
                                                                                                                                                                    /tissue_type="Retina"
/dev_stage="Adult"
/lab_host="EMDH10B"
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CN368821
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/clone_lib="NN0045"
//orlone_logan: nervous normal; Vector: puc18; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196.716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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1 (Dases 1 to 570)

Wistow,G. Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,

Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.

Expressed sequence tag analysis of human retina for the NEIBank Project: Retbindin, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts
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                                                                                                                                                                                                                                                                                                                                                                     391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 CACTGAGCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACCCCAGAATATCGAAGATGAAGC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACTGAGCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACCCCAGAATATCGAAGATGAAGC 451
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                                                                                                                                                                                                                                                                                                                                                       332 AGGACTTAAAGAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGCTGAGCCACA
                                                                                                                                                                                                                                                                                                                                                                                      30 AGGACTTAAAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGCTGAGCCACA
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                                                                                                                                                                                                                                                      17.9%; Score 415; DB 4; Length 444; llarity 100.0%; Pred. No. 5.9e-211; Conservative 0; Mismatches 0; Indels
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Section on Molecular Structure and Function
National Eye Institute MM 20892-2740, USA
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Plate: 17 row: b column: 04
Seg primer: M13RP1 reverse primer (ABI).
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Tel: 301 402 3452
Fax: 301 496 0078
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he17b04.yl Human Retina
Homo sapiens CDNA clone
BQ639558
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Matches 415; Conserv
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Gaps

1747

281

221

1807

341

1867

401

1927

461

1987

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1. .629
/organiam="Homo sapiens"
/orl_type="mRNA"
/db_xref="taxon:9606"
/clone="hw36h12"
                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                       pericytes
Unpublished (2004)
                                                                                                                                              Tel: 301 402 3452
Fax: 301 496 0078
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447; Conserv
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                                                                                                                                                                                                                          /tisgue_type="embryonic stem cell, retinoic acid and mitogen-treated hES cell line H7"
/clone lib="GRN PRENEU"
/note="oligo dT primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."
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 Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
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                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity 99.8
Matches 452; Conservative
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CN483754
                                                      JOURNAL
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undemprinted (1174), Vector: pSport1; RNA was extracted from /note="Organ: Eye; Vector: pSport1; RNA was extracted from primary human pericytes in culture. A directionally cloned primary human pericytes in culture. A directionally cloned constructed at Bioserve Biotechnology (Laurel MD) essentially following the protecols of the SuperScript plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pgArTAGATCAGAGGGGCGCCC(7)15-3'). CDNA was cloned in Not I/Sal I sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC)."
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                                                                                 Tsai,J.Y. and Wistow,G.
Expressed sequence tag analysis of cultured primary human ocular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCGCTCAGACAGGGAACAATTTCTAGGTCATATGAGAGGTTCCCTGCTTACCCTGCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell type="pericytes"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone lib="Human primary human ocular pericytes.
Unamplified (hw)"
Eukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Eutele:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 629)
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                                                                                                                                                                                      Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
                                                                                                                                                                                                                                                                6/331, NIH, Bethesda, MD 20892-2740, USA
                                                                                                                                                                                                                                                                                                                                               Email: graeme@helix.nih.gov
plate: 36 row: h column: 12
Seg primer: M13RP1 reverse primer (ABI)
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Homo sapiens (human)
Homo sapiens
Homo sapie
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                                                                                                                                                                                                            600 GAGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAG 659
                                                                                                                                                                                                                                                        377 GAAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCACA 318
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Email: asimpsonabludwig.org.br
This asimpsonabludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entrry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-101100-409-406&E53=2000-11-10&E4=1)
Seq primer: puc 18 forward
High quality sequence stop: 4.
Location/Qualifiers
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Fua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Somegraphics of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                720 GATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCATGATACAGATGATGATAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             540 GGAGAACCACAACAAGAGGATGATTTTTTTTTTTTGGCGACTGATGTTGATAGATTT
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/organism="Homo sapiens"
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AUTHORS
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// Organism="Homo sapiens"
// mol type="mRNA"
// moles factor for factor fac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 49)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Garvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Simpson, A.J.

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                        BQ340475 497 bp mRNA linear EST 20-MAY-2002 QV2-NN2006-110501-627-c09 NN2006 Homo sapiens CDNA, mRNA sequence.
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Fax: +55-11-2707001
Fax: +55-11-2707001
Emall: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN2006-110501-627-c09&t13=2001-05-11&t4=1)
Seq primer: pur 18 forward
High quality sequence stop: 496.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                    BQ340475
BQ340475.1 GI:21001375
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 553)

1 (bases 1 to 553)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Brunstein, A., deoliveira, P.S., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI035330
QV2-NNZ003-230401-624-a03 NNZ003 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    735 GTAGTAGAAGATGAAAGATTGCACCATGATACAGATGTAACATACCAAACATACCAAGATGTATGAG 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 72"
/note="Crgan: skin; Vector: pCMV-SPORT6; Site_l: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2 kb. Library constructed by Life
Technologies."
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                                                                                                                                                                                                                                                                                                           615 GAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGACAGTTTCACAAGAC
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                                                                                                                                                                                                                                      555 GAGGATGATTTTTTTTTTGCGACTGATGTAGATGATAGATTTGAGACCCTGGAACCT
                                                                                                                                                                                                                                                           sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                  Length 1031;
                                                                                                                                                                                                  0, Indels
                                                                                                                                                                  16.9%; Score 392; DB 5; Le
100.0%; Pred. No. 1.6e-198;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BI035330.1 GI:14441956
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Bit (Dases I to 1031)

Bit (Dases I to 1031)

In Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov/.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov/.

Contact: Robert ATCC/DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Blossience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Right quality sequence stop: 425.

High quality sequence stop: 425.
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AGENCOURT 7593740 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:60650475', mRNA Sequence.
         derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) poffiles into the PUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."
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                                                                                                                                         Length 503;
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100.0%; Pred. No. 3.5e-200;
ive 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="IMAGE:6065047"
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1...409. // Corganism - Homo sapiens" // Mol Lype="mRNA" | Ab_xref="taxon:9606" | // Ac_stage="Adult" | // Ac_stage="Adult" | // Ac_stage="Adult" | // Clone lib="Brofs!" | // Aria-lib="ary was made by cloning products derived from CRESTES PER (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 4019)
1 (Dases 1 to 4019)
1 Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Modai, M.A., de Silva, W. Jr., Eago, M.A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Singson, A.J.
                                                                                                                                                                                                                                                                                      Fax: +55-11-2707001
Email: animpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM0-BT0651-150
300-002-g05&t3=2000-03-15&t4=1)
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                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAGGTTCCTGTGGAGGCAGAACCCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 AGATGGACCCACAGGAGAACCACAAGAGGATGATGAGTTTCTTATGGCGACTGATGT
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                                                                                                                                                         Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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100.0%; Pred. No. 8.1e-195;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                             Seg primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 409
Location/Qualifiers
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                                                                                                                                                                                                                                                                            Tel: +55-11-2704922
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Best Local Similarity 100.0
Matches 385; Conservative
                                                                                                                                             sequence tags
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                       REFERENCE
AUTHORS
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BE084010 409 bp mRNA linear EST 12-JUN-2000 PMO-BT0651-150300-002-905 BT0651 Homo sapiens cDNA, mRNA sequence:
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                         CACTGAGCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACCCCCAGAATATCGAAGATGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 AGACTIGCAACAAGAAGAIGGACCCACAGGAGAACCACAACAAGAGGAIGAIGTITCT
                                                                                                                                                                                                                                                                                                                                                                                     332 AGGACTTAAAGAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGCTGAGCCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAAGAACAAATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   512 AGACTTGCAACAAGAAGATGGACCCACAGAGAACCACAACAAGAGGATGATGAGTTTCT
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Pred. No. 6e-197;
0; Mismatches 2; Indels
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BE084010.1 GI:8474363
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ilarity 99.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                             Similarity
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Best Local S
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/tissue_type="embryonic stem cell, retinoic acid and mitogan-treated hES cell line H7" /clone lib="GRN PRENBU" /note="foligo dT primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 TGAGGAAGTTCTAGGAAACTAGGAATCTATGATGCTGATGGTGATGAGAGATTTTGATGT 310
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1 (bases 1 to 46)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.M.

Lebkowski, J and Stanton, L.M.

Control human ES cell growth and differentiation

Mar. Bactechnol. 22 (6), 707-716 (2004)

Regenerative Medicine
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318 GGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC
                                       241 TIGITGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAG
                                                               361 CAGCAGTCCCGGCCAGAAGAGGCTGAGCCACACACTGAGCCCGAGGAGCAGGTTCCTGTGG
                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CN368831 46-MAY Linear EST 16-MAY 1inear EST 16-MAY 17000600846567 GRN_PRENEU Homo sapiens CDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 Constitution Drive, Menlo Park, CA 94025, Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 468 Std Error: 0.00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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CN368831
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/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/lab_host="DH10B"
/clone_lib="Lupski_dorsal_root_ganglion"
/clone_lib="Lupski_dorsal_root_ganglion"
/clone="vector: pCWV-SPORT6" (Life Technologies); Site_1:
Not1; Site_2: Sal1; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCACGCCTCG-3' and
5'-GACTAGTTCTAGATCGCGAGCGGCCCT(15)-3'. Size selected
5'-GACTAGTTCTAGATCGCGAGCGGCCCT(15)-3'. Size selected
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
Technologies."
                                                                                                                        BU838423
AGENCOURT 8123161 Lupski dorsal root ganglion Homo sapiens CDNA clone. IMAGE:6177038 5', mRNA sequence.
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I .M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMA13554 row: f column: 15
Plate: LLAMA13554 row: f column: 15
High quality sequence stort: 66
High quality sequence stop: 549.
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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16.5%; Score 383; DB.5; L
Best Local Similarity 99.4%; Pred. No. 1.1e-193;
Matches 533; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Organism="Homo sapiens"
|mol_type="mRNA"
|db_xref="taxon:9606"
|clone="IMAGE:6177038"
          BU838423.1 GI:24022818
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AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
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Homo sapiens by sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dasses 1 to 626)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Lib, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Transcription characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechhol. 22 (6), 707-716 (2004)
                                                                                                                                                                                                                                       1895 CACGCTGTGGCAGCAAGGAAGAAATGAAAATGCCTGCAAAGGAGCTCCTAAAAACCTG
                                                                                                                                                                                                                                                                                          TACCTTACTAGAAAAGTTCCCCGAGACAACAGGATGCAGAAGAGGACAGATCAAATATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                        2075 AAIGCACCTGGGCTTGGTGATTCCCAAGGAAGGCTGCAAGATTCGATGTGCCAACGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2135 CAGGACCTGGGAAGGAAGGCAAGGTGCTCATCTTTGATGACTCCTTTGAGCACGAGGTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 CAAGACCTGGGAGGAAGGAAGGTGCTCATCTTTGATGACTCCTTTGAGCACGAGGTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
        1996. For additional information, contact:
bentc-soares@uiowa.edu
TAG_TISSUB-Liung Epithelial Cells Tissue nos 359-368
TAG_IB=UI-CR-RNO
TAG_EGGCTGTAGGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CN368826 626 bp mRNA linear EST 16 17000424344515 GRN_EB Homo saplens CDNA 5', mRNA sequence.
                                                                                                                                            Length 720;
                                                                                                                                       Score 379; DB 6; Length 72
Pred. No. 1.5e-191;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 966
Email: rbrandenberger@geron.com
Insert Length: 626 Std Exror: 0.00.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .626 /organism="Homo sapiens"
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                                                                                                                                         16.3%;
ilarity 99.8%;
Conservative
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// Mol type="mRNN"
/ Clone="Ul_CF-FN0-aff-d-19-0-UI"
/ Lisbue type="Human Lung Epithelial cells"
/ Lab_host="DH10B (Life Technologies) (T1 phage resistant) "
/ Clone lib="Ul_CF-FN0"
/ Clone lib="Ul_CF-FN0"
/ Note="Organ: Lung; Vector: pTT3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UL-CF-FN0 is a subtracted cDNA library derived from two
normalized Human lung epithelial cell libraries (EN1 and
DU1) The library was subtracted according to according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA311352 720 bp mRNA linear EST 04-NOV-2002 UI-CF-FNO-aff-d-19-0-UI.81 UI-CF-FNO Homo sapiens cDNA clone UI-CF-FNO-aff-d-19-0-UI 3', mRNA sequence.
                                                                              186
                                                                                                                  490
                                                                                                                                 CGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCCACAGGAGAACCACA
                                                                                                                                                                                                                                                          247 CGCAGAACATGTTGAGGGAGAGACTTGCAACAAGAAGGAGGAGAAGCACACAGGAGAACCACA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: paul-mccray@ulowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Blosystems
Seq primer: M13 FORWARD
POLYA=Yes.
GGATGATGCCAAAGTTTTATTAGGACTTAAAGAGAGATCTACTTCAGAGCCAGCAGTCCC 126
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                 GCCAGAAGAGGCTGAGCCACACTGAGCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACC
                                                           CCAGAATATCGAAGGATGAAAAGGAACAAATTCAGTCCCTTCTCCATGAAATGGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 36 7771
Email: paul-mccray@uiowa.edu
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                                                                                                                                                                                                                                                                                                                                      611 ACCTGAAGTATCTCATGAAGAA 632
                                                                                                                                                                                                                                                                                                                                                                    367 ACCTGAAGTATCTCATGAAGAA 388
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1. .720
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CA311352.1 GI:24529450
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Homo sapiens
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/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/drisue_type="embryonic stem cells, embryoid bodies
derived_from | 1, H7 and H9 cells"
/clone lib="GRN_EB"
/note="oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE876059 1048 bp mRNA linear EST 20-OCT-2000
601485742F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887962 5',
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NIH-MGC http://wgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DrCIP/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                       AGCATGGAGGACACAAGAATGGGAGGAAAAGGCGGACTCTCGGGAACTTCATTCTTCACGT
                                                                                                                                                                                                                               1 CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCAGCGGCAACAGCAGCAGCAGCG
                                                                                                                                                                                                                                                    GGTTTATIGGTGATTGCTTGGCGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAG
                                                                                                                                                                                                    Gaps
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0
                                                                                                                                                                     Length 626;
                                                                                                                                                                                                    1; Indels
                                                                                                                                                                       Score 370; DB 7;
Pred. No. 1e-186;
0; Mismatches 1;
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BE876059 GI:10324835
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99.8%;
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Homo sapiens
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20; Conservative
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                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3887962"
/tissue_type="large cell_carcinoma, undifferentiated"
/lab_hogt="pH10B (phage-resistant)"
/clone lib="NHH MGC 69"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
/reflectionally. Primer: Oligo dT.
// Average insert size 1.1 kb. Library constructed by Life
Technologies."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. washU-NCI human EST Project
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1
  Plate: LLAM9667 row: d column:
                 High quality sequence stop: 670.
Location/Qualifiers
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                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammallai, Eutheria; Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 393)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L.W.

Transcriptome characterization elucidates signaling networks that control human Es cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
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         17000600014160 GRN_PRENEU Homo sapiens cDNA'S', mRNA sequence.
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llarity 100.0%; Pred. No. 5.4e-162;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                               Regenerative Medicine
Geron Corporation
Tel Constitution Drive, Menlo Park, CA
Tel Sco 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 393 Std Error: 0.00.
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/organism="Homo sapiens"
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                           CN368818
CN368818.1 GI:47368752
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Homo sapiens
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      Unpublished (1997)

Contact: Wilson RK
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Best Local Similarity 100.0%; Pred. No. 4.1e-164;
Matches 328; Conservative 0; Mismatches 0; Indels
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Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
Sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                   AL694159
527 bp mRNA linear EST 04-SEP-2003
DKFZp31311441 rl 313 (synonym: hlcc2) Homo sapiens cDNA clone
DKFZp313D1441-5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAATCCTGTAGAAGATTCACAGGTAATTGTAGAAGAAGTAAGCATTTTTCCTGTGGAAGA 925
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1 (bases 1 to 527)

Koehrer,K., Beyer,A., Mewes,W., Weil,B. and Wiemann,S.
EST (Koehrer,K., Beyer,A., Mewes,H.W., Weil,B. and Wiemann,S.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hlcc2)"
Site_1: SfiIA; Site_2: SfiIB;
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No s1 sequence available.

This clone (DKFZp313D1441) is available at the RZPD in I Please contact the RZPD: Ressourcenzentrum, Heubnerweg (Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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100.0%; Pred. No. 2.3e-160;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="DKRZp3131441"
/dev_stage="adult"
/lab_host="DH108"
/clone_lib="313 (synonym: h./note="Vector: priplibEx2; s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.527
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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515 CAGCAGTCCCGCC 527
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Vice = "Organ: Eye; Vector: pSport1; RNA was extracted from primary human pericytes in culture. A directionally cloned cDNA library in the pSporTI vector (Invitrogen) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the proteocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pgAcTAGATCTCGAGGGGCCCC(T)15-3']. CDNA was cloned in Not I/Sal I sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC)."
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                                                             Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                   1 (bases 1 to 580)
Tsai,J.Y. and Wistow,G.
Expressed sequence tag analysis of cultured primary human ocular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 CGGACCGTGCAATGGCCCCAGCGTAAGAATGCCAAGAGCAGCGGCAACAGCAGCAGCAGC
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/dev_stage="Adult"
/lab_host="EmbH10B"
/clone_lib="Human primary human ocular pericytes.
Unamplified (hw)"
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                                                                                                                                                                                                                     Section on Molecular Structure and Function
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llarity 99.7%; Pred. No. 6.9e-161;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                         National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
                                                                                                                                                                                                                                                                                                                Email: graeme@helix.nih.gov
Plate: 05 row: d column: 04
Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:9
clone="hw05d04"
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                                 Homo sapiens (human)
                                                                                                                                                                     pericytes
Unpublished (2004)
                                                                                                                                                                                                       Contact: Wistow G
                                                                                                                                                                                                                                                                               Tel: 301 402 3452
                                                                                                                                                                                                                                                                                                   Fax: 301 496 0078
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Matches 372; Conserv
                                                   Homo sapiens
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             KEYWORDS
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1. .484
//crganism="Homo sapiens"
//mol_type="mRNA"
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//lab host="DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 1 (Dases I to 484)

13 Ebett,L., Hell,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,

14 Radelof,U., Schneider,D. and Korn,B.

15 Human Uniquescete - RZPD3

16 Contact: Ina Rolfs

17 Rapp Deutesches Resourcenzentrum fuer Genomforschung GmbH

18 RZPD Deutesches Resourcenzentrum fuer Genomforschung GmbH

18 RZPD: INAGOBOSTO-69120 Heidelberg, Germany

19 RZPD: INAGOBOSTO-69120 Heidelberg, Germany

19 RZPD: INAGOBOSTO-69120 Heidelberg, Germany

19 RZPD: INAGOSTO-69120 Heidelberg, Germany

10 RZPD: INAGOSTO-69120 Heidelberg, Germany

10 RZPD: LASPO-69120 Heidelberg, Germany

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11 RZPD: Germany

11 RZPD: Germany

12 RZPD: Heidelberge: TriColor Germany

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14 RZPD: Germany

15 RZPD: Germany

16 RZPD: Germany

17 RZPD: Heidelberge: TriColor Germany

18 RZPD: Germany

19 RZPD: Germany

10 
                                                                                                                                                                                                                      BX111251 484 bp mRNA linear EST 07-FEB-2003
BX111251 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGP998F034597 ;
IMAGE:1876994, mRNA sequence.
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Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 484)

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1244 ATTTCCC 1250
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                                                                                                                               2023 bp DNA linear GSS 16-DEC-2003 Pan troglodytes ASPH gene, VIRTUAL TRANSCRIPT, partial sequence,
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todak, A.G., Glanowski, S., Nielson, R., Lu, F., Murphy, B., Todak, A.G., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 302 (5652), 1960-1963 (2003)
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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                                                                       RESULT 62
AY405268
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Homo sapiens (human)
Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 682)
Si NIH-MGC http://mgc.nci.nih.gov/.

I (bases 1 to 682)
Si NIH-MGC http://mgc.nci.nih.gov/.

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I (base 1 to 682)

I (contact: Robert Straubberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.E. Consortium/Link at:

http://image.llnl.gov

Plate: LLAM10169 row: h column: 15
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/mol_type="mRNA"
/do xref="taxon:9606"
/clone="IMAGE:4424894"
/tissue_type="hypernephroma, cell line"
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/clone=line"NIH MGC 89"
/clone=lorgan: kidney; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                        AGACTATTAAAGCTGGAACTTGATGCTGCAGAAAAACTCCGTAAAAAGGGGAAAAATTGAGG 1086
                                                                                                                                                                                                                                                                                           1087 AAGCAGTGAATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAGTCCACGAGCAAGAT 1146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG170148 682 bp mRNA linear EST 06-FEB-2C 602321860F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4424894 5', mRNA sequence.
                                                                                                                                                                                                                       179 AGACTATTAAAGCTGAACTTGATGCTGCAGAAAACTCCGTAAAAGGGGGAAAAATTGAGG
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BG170148
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Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
761: 319 335 9256
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Louis Staudt
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
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DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   503 bp mRNA linear EST 09-SEP-2003
UI-HF-BNO-anb-d-05-0-UI.x1 NIH MGC_50 Homo sapiens cDNA clone
MAGE:3092001 5', mRNA sequence.
                                                                                                                                                                                                         1088 AGCAGTGAATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAGTCCACGAGCAAGATA 1147
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                                                                          GACTATTAAAGCTGAACTTGATGCTGCAGAAAACTCCGTAAAAGGGGAAAAATTGAGGA 1087
                                                                                                                                                                                                                                                    241 AGCAGTGAATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAGTCCACGAGCAAGATA 300
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 503)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                 0; Gaps
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452 424

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CR559422 737 bp mRNA linear EST 14-JUL-2004 DKF2p4681163 x1 468 (synonym: phrtl) Pongo pygmaeus cDNA clone DKF2p4681163 5', mRNA sequence. CR559422 CR559422. GI:50298874
                                                                                     GGAATCTATGATGCTGATGGTGATTTTTGATGTGGATGATGCCAAAGTTTTATTA 332
                                                                                                                                                                   AAAGAACAAATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAA 512
                                                                                                                                                                                                                                                                                                                                                                                               /ugailame...rousy prymmacus
/mol_type="mixMa" / db xref="taxon:9600"
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/tisme_type="heart"
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/lab_host="Dh10B"
/clone_lib="468 (synonym: phrt1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKF2);
Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen
(Hilden/Germany) within the CDNA sequencing consortium of the
German Genome Project. This clone (DKF294681163) is available at
the RZPD Deutsches Resourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contect RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKF294681163
Further information about the clone and the sequencing project is
available at http://mips.gff.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pongo pygmaeus (orangutan)
Pongo pygmaeus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                                                                                                             393 ACTGAGCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACCCCCAGAATATCGAAGATGAAGCA
                                                                                                                                                                                                                                                                                                                       ACATCTGTAGCTGTCGTTTGGTTTGATCTTGAGGAAGTTCTAGGAAAACTA
                                                                                                                                                                                                                     GGACTTAAAGAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGCTGAGCCACAC
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Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Forgo, pygmaeus mid Wiemann, S.
Pongo, pygmaeus May (Bahr, A., Lauber, J., Mewes, H.W., et al.)
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Pongo pygmaeus"
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MIPS
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DKFZp4691163_r1 469 (synonym: pkidl) Pongo pygmaeus cDNA clone
DKFZp4691163_s', mRNA sequence.
                     749
                                                                                                                                                  810 GAACCTCTAGAAAATGAAGGGATAGAAATCACAGAAGTAACTGCTCCCCCTGAGGATAAT 869
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                                                                                                                                                                                                                                                                          527
                                                                                                                                                                                                                                                                                                                              This is the 5' sequence of the clone insert clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg de; sequenced by Qiagen (Hilden/Germanny) within the CDNA sequencing consortium of the German Genome Project. This clone (DKFZp4691163) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:

http://www.rzpd.de/cgi.bin/products/cl.cgi?Clone1D=DKFZp4691163

Further information about the clone and the sequencing project is available at http://mips.gf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 GGACTCTCGGGAACTTCATTCTTCACGTGGTTTATGGTGATTGCATTGCTGGGCGTCTGG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammallai; Butheria; Primates; Catarrhini; Hominidae; Pongo.
1 (bases 1 to 719)
Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
Pongo pygmaeus mRNA (Bahr, A., Lauber, J., Mewes, H.W., et al.)
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
GAAACCGAGCATAGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATG
                                                                     690 GAAGAGATGTCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGAA
                                                                                                                                                                                                                                                    870 CCTGTAGAAGATTCACAGGTAATTGTAGAAGAAGTAAGCATTTTTCCTGTGGAAGAACAG
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/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db xref="taxon:9600"
/clone="DKPZp4691163"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pongo pygmaeus (orangutan)
Pongo pygmaeus
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Length 737; Score 308; DB 7; I Pred. No. 2.5e-153; 13.3%; Query Match Best Local Similarity

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plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pdacTAGTTCTAGATCGCGAGCGCCC(T)15-3']. cDNA was cloned in Not I/Sal I sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells" /clone_lib="GRN_EB" /note="oligo dT_primed, full-length enriched cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 TIGITGACTATGAGGAAGTICTAGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 548)

Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,

Lebkowski,J. and Stanton,L.W.

Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation

Nat. Biotechnol. 2 (6), 707-716 (2004)

Contact: Brandenberger R.

Regenerative Medicine
                                                                                                                                                                                                                                                                                                                                   GCTCCGGCAGGGTAGCACGAGGAGCAGCAGCAGCCCCGGGGGCCCCGGAGAGAGACAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTITICATIGIAGICALICALAGITITIATTAGGACTTAAAGAGAGATCTACTTCAG 357
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17000424344539 GRN_EB Homo sapiens CDNA 5', mRNA sequence.
CN368828
                                                                                                                                                                             Length 560;
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230 Constitution Drive, Menlo Park, CA 94025,
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 548 Std Error: 0.00.
Location/Qualifiers
                                                                                                                                                                             13.2%; Score 306; DB 7; I
llarity 99.7%; Pred. No. 2.8e-152;
Conservative 0; Mismatches 1;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CN482623

bw22f04.yl Human primary human ocular pericytes. Unamplified (hw) mRnA sequence.

CN482623.1 GI:46564127
                                                                                                                                                                                                                                                                                      GGACTTAAAGAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGCTGAGCCACAC 392
                                                                                                                                                                                                                                                                                                                                                                 393 ACTGAGCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACCCCCAGAATATCGAAGATGAAGCA 452
                                                                                                                                                                                                                                                                                                                                                                                                                                             453 AAAGAACAAATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAA 512
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                                                                                                                                                                                                          GGAATCTATGATGCTGATGGTGATTTTTGATGTGGATGATGCCAAAGTTTTATTA 332
                                                                                                                                                                                                                                                   304
                                                                                                                                                                                                                                                                                                              165 ACTGAGCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACCCCAGAATATCGAAGATGAAGCA 424
                                                                                       GGACTCTCGGGGAACTTCATTCTTCACGTGGTTTATGGTGATTGCATTGCTGGGGGTCTGG 184
                                                                                                                                                                       244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryora, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I, Dases I to S60)
Tsai, J. Y. and Wistow, G. Expressed sequence tag analysis of cultured primary human ocular
                                                                                                                                                                                                                                  245 GGAATCTATGATGCTGATGGTGATGGAGATTTTGATGTGGATGATGCCAAAGTTTATTA
                                                                                                                                213 ACATCTGTAGCTGTCGTTTGGTTTGATCTTGACTATGAGGAAGTTCTAGGAAAACTA
                                                                                                                                                                   Acercieracierecerriegricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: graemeehelix.nih.gov
Plate: 2z row: f column: 04
Seq primer: Mi3RP1 reverse primer (ABI).
Location/Qualifiers
1.560
/organism="Homo sapiens"
/mol type="mRNA"
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/cell type="pericytes"
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/lab hose stage="RMAult"
/lab hose stage="RMAult"
/lab hose libe="HMBH108"
/clone lib="Human primary human ocular pericytes.
/unamplified (hw)"
                                                     GGACTCTCGGGAACTTCATTCTTCACGTGGTTATGGTGATTGCATTGCTGGCGTCTGG
                Gaps
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                  Indels
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Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
TTE1: 301 402 3452
Fax: 301 496 0078
                  5;
                    Mismatches
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Homo sapiens
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Unpublished (2004)
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CN482623
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EST 16-MAY-2004

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Eukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (Bases 1 to Sprimates; Catarrhini; Hominidae; Homo.

El (Bases 1 to Sprimates; Catarrhini; Hominidae; Homo.

Es Kim,N.S., Hahn,Y.; Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

Contact: Kim YS

Genome Research Institute of Bioscience & Biotechnology

S. Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-8
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Kr EST7064453 S9SNUG01 Homo sapiens cDNA clone S9SNUG01-34-C04 5',
mRNA sequence.
BM785890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / tissue type="Ascites"
/cell_type="Epithelial"
/cell_line="SNU-601"
/lab_host="Tropip""
/clone_lib="S9SNU601"
/note="Organ: Stomach; Vector: pME18-FL3; Site_1: Xho1;
                                                                                                                                                                                                                                                                                                                                                                                       61 GTGGCCGCACACAGGCCCCACAAACTGCAGGCTCCGAATGCACCTGGGCTTGGTAGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2039 GTGGCCGCACACAGGCCCACAAACTGCAGGCTCCGAATGCACCTGGGCTTGGTGATTCC
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                     Average insert size 1.4 kb. Library prepared by Life Technologies."
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                                                                                                                                    Length 509;
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                                                                                                                                 Score 295; DB 2; 1
Pred. No. 2.3e-146;
0; Mismatches 1;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S9SNU601-34-C04"
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Similarity 99.7%;
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SM Homo sapiens (human)
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Homo sapiens
Homo sapiens
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 509)
I (bases I to 509)

Mational Institutes of Health, Mammalian Gene Collection (MGC)
Mational Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: capable-remail.inh.gov
Tissue Procurement: APCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 447.
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
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                                                                                                                                                                                                                                                                                  GGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC 240
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/mol type="mRNA"
/db_xef="taxon:90e"
/db_xef="taxon:90e"
/clone="INAGE:304836"
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/tlab_host="DH108"
/clone_lib="NIH MG"
/clone_lib="NIH MG"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI; Site=2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                                                                      CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCAGCGGCAACAGCAGCAGCAGCG 60
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                                                                                                                                                Length 548;
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Best Local Similarity 99.7%; Pred. No. 1.9e-147;
Matches 347; Conservative 0; Mismatches 1;
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Site 2: Xhol; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including Sit site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using Sfil oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with Sfil and cloned into DraIII - digested pMR18S-FIJ vector. The obtained cDNA vectors were used for transformation of competent cells E. coll TOPLOF, by electroporation method. The CDNA libraries constructed by this method are full-length enriched CDNA library."
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AV751514
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1 (bases 1 to 622)
Song, H., Peng, Y., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, Y., Gao, X., Cheng, Z., Xi, Z., Zeng, L., Xu, S., Chang, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Ye, M., Han, Z., Chen, Z., Hu, R. and Chen, J.

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           568 ITCTIATGGCGACTGATGTAGATGATAGATTTGAGACCCTGGAACCTGAAGTATCTCATG 627
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                                                                                                                                                                                                                                                                                                                                                                                                                          508 GAGAAGACTTGCAACAAGAAGATGGACCCACAGGAGAACCACAACAAGAGGATGATGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 AAAGATTGCACCATGATACAGATGTGTAACATACCAAGTCTATGAGGAACAAG
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351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
Location/Qualifiers
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Shanghai Institute of Endocrinology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64370045(ex.663332)
Fax: 86-21-64743206
Email: mbshi@ms.stn.sh.ch.
                                                                                                                                                                                                                                                                                                                                           12.7%; Score 294; DB 4; Length 536; 100.0%; Pred. No. 8e-146; Pred. 0; Mismatches 0; Indels
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/mol_type="mRNA"
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Matches 294; Conservative
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ENKARYOFGE, MELAZOA; Chordata; Craniata; Vertebrata; Euteleostomi; Enkaryofge; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 862)

INIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 RM10A07 Bethesda, MD 20892

Email: gapbs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

CDNA Library Preparation: CLONTECH Laboratorium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Plate: NDCM195 row: a column: 02

High quality sequence $\frac{\text{stop}}{\text{stop}} = \frac{\text{stop}}{\text{stop}} = \frac{\text{stop}}
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                                                                                                                             /clone lib="NPD"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
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AGENCOURT 14354806 NIH MGC_186 Homo sapiens cDNA clone IMAGE:30406369 5', mRNA sequence.
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12.7%; Score 294; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 8.2e-146;
Matches 294; Conservative 0; Mismatches 0;
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/clone="NPDAXB01"
/tissue_type="pituitary"
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/lab_host="SOLR"
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Homo sapiens
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/note="Organ: Pooled-Skin, Vector: pDNR-LIB; Site 1: Sfil (ggocacteggoc); Library is oligo-cattratgaco; Site 2: Sfil (ggocacteggoc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a pooled samples of tissues from Skin, meninges, duramatter, pia matter and choroid plaxus. S, and aptors were used in cloning as follows: S, adaptors were used in cloning as follows: S, adaptor sequence: S'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: S'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: S'-CACGGCCATGATGGCCC-3' or T). Average innert size 1.47 kb (range o.50-4.0 kb). IS/1S colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Liboraty".
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Bu lbases 1 to 1010; Brimates; Catarrhini; Hominidae; Homo.

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Charary Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLAM12236 row: e column: 02

High quality sequence stop: 579.
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Homo sapiens cDNA clone IMAGE:5540329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        833 AGAAATCACAGAAGTAACTGCTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAAT 892
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Best Local Similarity 100.0%; Pred. No. 8.7e-146;
Matches 294; Conservative 0; Mismatches 0;
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1 (Dases 1 to 767)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L.W.

Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
               /tissue_type="melanotic melanoma"
/lab.host="NHH WGC 72"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2 kb. Library constructed by Life
Technologies."
                                                                                                                                                                                                                                     1 CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCAGCGGCAACAGCAGCAGCAGCG
                                                                                                                                                                                                                                                                  CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCAGCGGCAACAGCAGCAGCG
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17000533684042 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
CN368820
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0
                                                                                                                                                                    Length 1010;
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al Similarity 99.5%; Pred No. 1.5e-142;
388; Conservative 0; Mismacches 2; Indels
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230 Constitution Drive, Menlo Park, CA 94025, USA
716: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 767 Std Error: 0.00.
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/mol_type="mRNA"
/clone="IMAGE:5540329"
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Homo sapiens
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Best Local S:
Matches 388
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CN368820
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/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived_from H1, H7 and H9 cells"
/clone_lib="GRN_BB"
/note="boligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
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                                                                                                                                                                                                                                                 180 CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCAGCGGCAACAGCAACAGCAGCAGCG 239
                                                                                                                                                                                                                                                                                           61 GCTCCGGCAGCGCACGACGAGCAGCAGCAGCAGCCCCGGGGCCCCGGAGAGAGACAA 120
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                                                                                                                                                                Query Match
12.2%; Score 283; DB 7; Length 767;
Best Local Similarity 99.7%; Pred. No. 7.1e-140;
Matches 333; Conservative 0; Mismatches 1; Indels
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Search completed: March 25, 2005, 22:28:27 Job time : 6796 secs

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21 104 4.5 592 1 22 72 3.1 1382 2 23 72 3.1 1382 8 24 72 3.1 1382 8 25 72 3.1 1382 8	25 2208 113 2.5 2208 13 59 2.5 2208 13 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	31 27 1.2 27 1.3 32 23 1.3 22 0.9 855 4 34 22 0.9 1933 4 34 22 0.9 1933 4 35 20 0.9 1933 4 35 20 20 20 20 20 20 20 20 20 20 20 20 20	22 0.9 2855 4 22 0.9 3705 4 3 22 0.9 3933 4 22 0.9 3974 4	22 0.9 5903 4 1 21 0.9 1845 3 21 0.9 1845 3	21 0.9 4011 2 2 20 0.9 20 4 2 2 2 0 0.9 2 2 0 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	48 20 0.9 20 8 50 20 8 50 20 9 20 8 51 20 0.9 52 113 55 20 0.9 55 113 55 20 0.9 55 0 123	20 0.9 786 11 20 0.9 849 2 20 0.9 908 3 20 0.9 908 5	20 0.9 984 4 20 0.9 1038 13 20 0.9 1038 13 20 0.9 1070 4 20 0.9 1088 13 20 0.9 1088 13	20 0.9 1109 2 20 0.9 1230 3 20 0.9 1245 12 20 0.9 1245 12 20 0.9 1418 10	70 20 0.9 1891 12 71 20 0.9 2000 8 72 20 0.9 2000 12	20 0.9 2370 20 0.9 2370 20 0.9 2803 20 0.9 3008 20 0.9 3144	78 20 0.9 3224 4 79 20 0.9 3369 13 80 20 0.9 3689 13 81 20 0.9 4021 4 82 20 0.9 4275 4	~	90 20 0.9 10531 8 ABZ4286 91 20 0.9 10694 11 ADL225 92 20 0.9 17951 4 ABL1184 93 20 0.9 24370 10 ADC864
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	Run on: March 25, 2005, 14:29:03 ; Search time 1157 Seconds (without alignments) 11890.647 Million cell updates/sec	Title: US-09-436-184-3 Perfect score: 2324 Sequence: 1 oggacogtgoaatggoccagttgggaaactctggagaga 2324	Scoring table: OLIGO_NUC Gapop 60.0 , Gapext 60.0 Searched: 4390206 segs, 2959870667 residues	Word size : 0 Total number of hits satisfying chosen parameters: 8780412	um DB seq length: 0 um DB seq length: 200000000	Database: N Geneseq11600000:* 1: geneseq119000:*	geneseqn2000s: geneseqn2001as geneseqn2001bs geneseqn2002as	geneseqn2003as: geneseqn2003bs: geneseqn2003cs geneseqn2004as geneseqn2004as	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Result Query No. Score Match Length DB ID Description	2324 100.0 2324 4 AAF89811 2324 100.0 2324 8 ABS57868 2324 100.0 2324 9 ADA00640 2222 95.6 2452 13 ADP23914	222 95.0 492 13 AUX9/34/ 221 93.4 5358 10 ADJ56257 895 38.5 2680 6 ABX04178 895 38.5 2680 13 ADP24208 640 27.5 2442 2 AAZ23609		459 19.8 502 9 ACH47067 359 15.4 660 6 ABG95507 249 10.7 495 11 ADT94758 104 4.5 161 12 ACH93769

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hydroxylase (HAAH) enzyme. Epidermal growth factor (EGF)-like domains of
colypeptides are hydroxylated by HAAH enzymes. HAAH is used in the method
of the invention. The specification describes a method for diagnosing a
conditions in a mammal. The method comprises contacting a body
fluid with an antibody which binds to HAAH polypeptide under complex
conditions, and detecting the antigen-antibody complex. The
condity fluid e.g. central nervous system (CNS)-derived body fluid, blood,
serum, urine, saliva, sputum, lung effusion, and ascites fluid of mammal,
where the neoplasm is derived from endodermal tissue and is selected from
colon cancer, breast cancer, pancreatic cancer, liver cancer, cancer of
bile ducts, and cancer of the CNS. HAAH antibodies, linked to a cytotoxic
agent, are useful for killing tumour cells
Add45153 Human gen
Aak84729 Human imm
Aak85983 Human imm
Aak84730 Human imm
Aak865984 Human imm
                                                                                                                                                                                                                                                                                                                     '*tag= a
'product= "human aspartyl (asparaginyl) beta-hydroxylase"
                                                    Acn43934 Human gen
Abg88126 Human ost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosing malignant neoplasm in a mammal, involves contacting mammalian sample with antibody that binds to human aspartyl beta-hydroxylase polypeptide to form antigen-antibody complex and detecting the complex.
                                                                                                                                                                                                                                        Epidermal growth factor-like domain; EGF-like domain; cancer;
human aspartyl beta-hydroxylase; HAAH; malignant neoplasm; tumour;
                                                                                                                                                                                                                   cDNA encoding human aspartyl (asparaginyl) beta-hydroxylase (HAAH)
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100.0%; Score 2324; DB 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2324; Conservative 0; Mismatches 0;
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The invention relates to diagnosing a neoplasm and inhibiting tumour growth in a mammal, using an antibody that binds to human aspartyl (asparaginyl) beta-hydroxylase (HAAH). Diagnosing a neoplasm comprises contacting a tissue with a detectably-labelled antibody where an increase in level of antibody binding at tissue site compared to the level of binding to normal non-neoplasmic tissue indicates the presence of a neoplasm at the tissue site. Inhibiting tumour growth in mammal involves administering the antibody conjugated to a cytotoxic agent to a mammal. Also included are a method of conferring an immune response to a tumour cell in a mammal, by administering the antibody, a method of inducing an HAAH-specific immune response in a mammal, an HAAH polypeptide (or a polynuclectide composition encoding the mammal polypeptide, or its degenerate variant), a fragment of HAAH comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; se; gene; aspartyl (asparaginyl) beta-hydoxylase; HAAH; cytostatic; immunostimulant; antibody; neoplasm; tumour; PB50; 86A; 5C7; 19B; brain tumour; glioma; glioblastoma; astrocytoma; haemangioma; pancreatic carcinoma; colon cancer; breast cancer; pancreatic cancer; liver cancer; cancer of the bile ducts; primary malignant CNS neoplasm; metastatic CNS neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosing neoplasm and inhibiting tumor growth, by contacting tissue of mammal with detectably-labeled antibody which binds to human aspartyl (asparaginyl) beta-hydroxylase.
       TATTCATCGTGGATGTGGCCATCCGGAACTGACACCACAGCAGAGGACGCAGAGCTTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA encoding aspartyl (asparaginyl) beta-hydoxylase, HAAH.
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(DEUT/) DEUTCH A H.
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cc antibody or its fragment which binds to HAAH, where the antibody is FB50, antibody or its fragment which binds to HAAH (where the antibody is FB50, CC or 198), a hybridoma cell line chosen from hybridoma FB50, HA366A, HA15CA and HA219B, and a fragment of HAAH which lacks enzymatic activity or alpha-keroglutarate binding domain and epidermal growth cartority or alpha-keroglutarate binding domain and epidermal growth in a mammal, conferring an immune crasponse to a brain tumour growth in a mammal, conferring an immune crasponse to a brain tumour cell (e.g. glioma, glioblastoma, astrocytoma or haemonican) in a mammal, for conferring immune response to a pancreatic carcinoma cell and for inducing a HAAH-specific immune crasponse in a mammal. The method is useful for diagnosing malignant concer, pancreatic cancer, liver cancer and cancer of the bile ducts. The method is also useful for diagnosing neoplasms of central nervous system (CNS) e.g. primary malignant CNS neoplasms of both neuronal and glial conciliant and metastatic CNS neoplasms, and for diagnosing brain tumours e.g. glioma, glioblastoma, astrocytoma or haemangioma. The cumours e.g. grimma, HAAH astrocytoma or haemangioma. The
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                                                                                                                                                                                  The present invention relates to a method for inhibiting tumour growth is a mammal, The method comprises administering to the mammal a compound, which inhibits the expression or enzymatic activity of a human aspartyl (asparaginyl) beta-hydroxylase (HAAH). The compound may inhibit HAAH hydroxylation of a NOTCH polypeptide. In particular, the compound may inhibit hydroxylation of an epidermal growth factor (EGF)-like repeat sequence in a NOTCH polypeptide. The methods are useful for inhibiting tumour growth or killing tumour cells, or for diagnosing or neoplasm is colon cancer, breast cancer, particular, the tumour or neoplasm is colon cancer, breast cancer, particular, the tumour or neoplasm is colon cancer, breast cancer, particular, the central nervous system (CNS). The present sequence encodes HAAH.
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                                                                           Inhibiting tumor growth or killing tumor cells (e.g. cancer of the cobreast, pancreatic, liver or the central nervous system), by administering an inhibitor of the human aspartyl (asparaginyl) beta-
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                                                                                                                                                                                                                                                                                              AAAACCTGAGGGAAAAAAGGGGGACTGGGGTTCACGCTGTGGCAGCAAGAAGAAGAA
                                                                                                                                                                                             CAACAGGATGCAGAAGAAGAACAGATCAAATATTCCATGCACCCCGGGACTCACGTGT
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(DMON/) DE LA MONTE S M.
(INCE/) INCE N.
(CARL/) CARLSON R I.
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CTTCCTGCCTGAGGATG 1860 AGAAAAGTTCCCCGAGA 1980 CCCCGGGACTCACGTGT 2040 regectregrartccca 2100 3GGAGGAAGGCAAGGTGC 2160 ||||||||||||||||||||||||3GGAAGGTGC 2160 CCTCATCTTCCGGCTGA 2220 AGAGACGCAGCCTTCCAG 2280 irheumatic; cological; ropic; respiratory; PM, Wood WI; GA 2324 || GA 2324

The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiatherhitic, antirheumatic, immunosuppressive, antiatherhitic, antirheumatic, immunosuppressive, coffeeopathic, antidabetic, dermatclogical, antipocriatic, antialergic, antiathermatic, hepatotropic, and respiratory activity A polymocleotide of the invention may have a use in gene therapy. The PRO polypeptide, its coffeeopathic, antagonist, or antibody that specifically binds to the property of properties, and properties is useful for treating an immune related disorder such as systemic lubus erythemacous, rheumatoid arthritis, osteoarthritis, osteoarthritis, a spondyloarthropathy, systemic sclerosis, and idopathic inflammatory myopathy, Siggren's syndrome, systemic classes, autoimmune haemolytic anaemia autoimmune contained thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous can be contained to the central or peripheral nervous can chromic inflammatory demyelinating polymeuropathy, duillain-Barre syndrome, a chromic inflammatory demyelinating polymeuropathy, a hepatobiliary cirrhosis, granulomatous hepatitis, sclescasing primary cirrhosis, granulomatous hepatitis, sclescasing primary cirrhosis, granulomatous hepatitis, sclescasing primary cirrhosis, granulomatous hepatitis, sclescasing contact dermatitis, food disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, a bulleagic ribinitis, atopic dermatitis, food changitis, contact dermatitis, food changitis, contact dermatitis, food changitis, schonophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity, urricaria, an immunologic disease of the lung, contact dermatitis, schecosing changing of the invention or the present sequence encodes a PRO protein of the invention. New PRO polypeptides and polynucleotides, useful for treating e.g. erychematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral nervous system. Claim 1; SEQ ID NO 1092; 2940pp; English P-PSDB;

Sequence 2452 BP; 779 A; 507 C; 657 G; 509 T; 0 U; 0 Other;

126 180 246 240 306 300 360 426 420 486 AGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG 480 CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCAGCGGCAACAGCAGCAGCAGC GGTTTATGGTGATTGCATTGCTGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC TTGTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAG **ATTITGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAAAGAGAGATCTACTTCAGAGC** CAGCAGTCCCGCCAGAAGAGGCTGAGCCACACACTGAGCCCGAGGAGCAGGTTCCTGTGG Query Match · 95.6%; Score 2222; DB 13; Length 2452; Best Local Similarity 99.9%; Pred. No. 0; Matches 2322; Conservative 0; Mismatches 2; Indels 0; Gaps -67 61 127 121 187 181 247 241 307 367 127 421 301 361 g ઠે ઠે g 8 8 S 8 6 8 6 8

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1140 1266 1026 1086 1506 1560 600 720 786 780 846 840 906 900 996 960 AGGCAGAAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG 546 967 AAGTAAGCATTTTTCCTGTGGAAGAACAGCAGGAAGTACCACCAGAAACAAATAGAAAAA AAATGGTACACGCAGAAACATGTTGAGGGAGAAGAACTTGCAACAAGAAGAAGAAGAAGAACCCCACAG GAGAACCACAACAAGAGGATGATGAGTTTCTTATGGCGACTGATGTAGATGATGATTTG ATTCCAGTGAACCAGTAGAAGATGAAAGATTGCACCATGATACAGATGATGTAACAT ACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAAAATGAAGGGATAGAAATCA CAGAAGTAACTGCTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG 1267 TGCTACGTGGAGCCATCGAGACCTACCAAGAGGTGGCCAGCCTACCTGATGTCCCTGCAG GAGAACCACAACAAGAGGATGATGAGTTTTCTTATGGCGACTGATGTAGATGATAGATTTG AGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGA CAGTITCACAAGACTGTAATCAGGATATGGAAGAGATGATGTCTGAGCAGGAAAATCCAG CAGAAGTAACTGCTCCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG CAGATGATCCAGAACAAAAAGCAAAAGTTAAGAAAAAAGAAGCCTAAAACTTTTAAATTAAAT TTGAGGAAGCAGTGAATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAGTCCACGAG TTGAGGAAGCAGTGAATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAGTCCACGAG AAATGGTACGCAGAACATGTTGAGGGAAGACTTGCAACAAGAAGATGGACCCACAG **ATTCCAGTGAACCAGTAGAAGATGAAAGATTGCACCATGATACAGATGAACAT** ACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAAAATGAAGGGATAGAAATCA CAAGATATGGGAAGGCGCAGTGTGAGGATGATTTGGCTGAGAAGAAGAAGTAATGAGG TGCTACGTGGAGCCATCGAGACCTACCAAGAGGTGGCCAGCCTACCTGATGTCCCTGCAG 1261 ACCTGCTGAAGCTGAGTTTGAAGCGTCGCTCAGACAGGCAACAATTTCTAGGTCATATGA ATGAAGAGCTGCTGAGTGTGACACCTAATGATGCTTTGCTAAAGTCCATTATGGCTTCA GAGGTTCCCTGCTACCCTGCAGAGATTAGTTCAACTATTTCCCAATGATACTTCCTTAA 1027 1021 1087 1147 481 547 541 607 601 667 199 727 721 787 781 847 841 204 901 961 1081 1207 1201 1141 1321 1387 1381 1447 1441 1507 1501 ò qq g ò ò БВ 8 8 8 8 4 8 6 8 6 8 6 8 6 8 ∂

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This invention relates to novel agents that modulates the function of human apoptosis-associated proteins specified within the specification. Specifically, it refers to a method for the identification of target genes whose expression is correlated with an early stage in the regulation of apoptosis. The present invention describes a method of contacting either candidate agents or control agents to the target genes and assessing the difference of binding and inhibitory activity, where the candidate agent is selected from a low molecular weight organic molecule, an antibody or fragment thereof, an antisense oligonucleotide, a small inhibitory dsRNA, or a ribozyme. As such, the compositions and methods are useful for diagnosing and treating diseases or conditions associated with abnormal apoptosis in mammalian tissue, such as cancer, inflammation, autoimmune or neurodegenerative disorders. Accordingly, than exhibit cytostatic, antiinflammatory, immunosuppressive and neuroprotective activities. These may also be used for drug screening purposes and in gene therapy. This polynucleotide sequence is a human than and the regulation of apoptosis that can be
                                                                                                                                                                                                                         Identifying an agent that modulates the function of an apoptosis-associated polypeptide, useful for diagnosing or treating e.g. cancer, comprises comparing the binding of the polypeptide to the candidate agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modulated by novel agents of the invention.
                                                                                                                                                                                                                                                                                                                  Claim 2; SEQ ID NO 55; 304pp; English.
                                                                                                      (EIRX-) EIRX THERAPEUTICS LID
                                                                  07-MAR-2003; 2003GB-00005267
                                 05-MAR-2004; 2004WO-GB000957
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P-PSDB; ADR97348.
16-SEP-2004
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                    CCGGAGATCCTGGCACTGATGATGGGAGATTTTATTTCCACCTGGGGGATGCCATGCAGA
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gene; ds; human; apoptosis; cancer; inflammation; autoimmune; neurodegenerative disorder; cytostatic; antiinflammatory; immunosuppressive; neuroprotective; gene therapy; ASPH;

beta hydroxylase.

aspartate

Homo

WO2004078783-A2 sapiens

Human ASPH DNA, an apoptosis related target Seq 55

(first entry)

ADR97347 standard; DNA; 2452

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TGCTACGTGGAGCCATCGAGACCTACCAAGAGGTGGCCAGCCTACCTGATGTCCCTGCAG
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                                                                                                                                                                                                                                                        This invention relates to novel isolated cDNAs that are differentially expressed in MYCN activated cells. Specifically, it refers to polynucleotide sequences that exhibit differential expression patterns in activated by the transactivator MYCN, where MYCN is a proto-concepene that is amplified in neuroblastoma cells and is common in small can use set useful for in hybridisation assays to detect expression of nucleic acids (or complementary nucleic acids) in a present in a given sample, as useful for in hybridisations exhibit coules or compounds that specifically bind the CDNA as a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also be used for gene therapy purposes. This polynucleotide sequence is a CDNA that is differentially expressed in MYCN activated cells, given in an exemplification of the invention. NOTE: This sequence does not appear in the printed specification but has been obtained in electronic format from the US Patent Office Atlantant Activity.
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                                                                                                                                                                                  New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the
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larity 99.9%; Pred. No. 0;
Conservative 0; Mismatches 3;
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(NUCH/) NUCHTERN J G.
(PLON/) PLON S E.
(SHOH/) SHOHET J M.
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              CCGCAGATCCTGGCACTGATGGGAGATTTTTATTTCCACCTGGGGGATGCCATGCAGA
                                         GGGTTGGGAACAAAGAGGCATATAAGTGGTATGAGCTTGGGCACAAGAGAGGACACTTTG
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The invention relates to new isolated nucleic acid molecule comprising a nucleic acid molecule consisting of a gene differentially expressed in cells undergoing differentiation from mesenchymal cell to a chondroblastic phenotype, or hybridiaing under stringent conditions to them (or their fragments). Also included are expression vectors, to the induce differentiation of a mesenchymal cell and may be used as an immunogen). Dinding partners of the polypeptides, a method for edentifying an agent useful in modulating mesenchymal cell and induction activity of a molecule, a method for a nucleic acid molecule or its expression product, a method for determining regression, progression or onset of cartilaginous tissue degeneration condition in a condition condition, a method for treating a cartilaginous tissue degeneration condition, a method for treating a cartilaginous tissue degeneration condition, a method for treating a subject to reduce the cisk of cartilaginous tissue degeneration condition developing in the cubect, an enthod for treating a subject to reduce the cisk of cartilaginous tissue degeneration condition, and a solid-phase nucleic acid molecule array consisting essentially of a set of nucleic acid molecule array consisting essentially of a set of nucleic acid molecule as cited above (or known from known genes shown to be condition, and a solid-phase nucleic molecule as cited above (or known from known genes shown to be condition, and agents and agents and agents are useful for treating cartilaginous tissue conditions such as observablymal cells using the technique of representational difference analysis, RDA), its expression products or tragments, fixed to a solid substrate. The nucleic acid of products or fragments, fixed to a solid substrate. The nucleic acid degeneration conditions such as observable and agents are useful for treating cartilaginous tissue degeneration and associated and agents are useful for treating cartilagines. The present sequence is a cDNA from a known gene differentially expres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecules capable of promoting chondrogenesis, useful for diagnosing and treating cartilaginous tissue degeneration conditions, e.g. osteoarthritis, rheumatoid arthritis, gout arthritis, or osterochondrosis.
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New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral

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Van Lookeren M, Williams PM,

Schoenfeld J,

Clark H, Wu TD;

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WPI; 2004-419628/39

P-PSDB; ADP24209

nervous system.

01-NOV-2002; 2002US-0423394P 30-OCT-2003; 2003WO-US034312

(GETH) GENENTECH INC

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                                                                                                                                      PRO polypeptide encoding cDNA SEQ ID NO:1386.
                                                                  ADP24208 standard; cDNA; 2680
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18-NOV-2004

ADP24208;

RESULT 8 ADP24208

WO2004041170-A2 Unidentified

21-MAY-2004

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polypeptide encoded by it. A protein of the invention has antifinflammatory, antiarthritic, antiphorition has antiantalergic, osteopathic, antidathitic, antiphoritatic, immunosuppressive, contemporation, antidathitic, antiphoritatory activity. A polymuclectide antiantmatic, hepatotropic, and respiratory activity. A polymuclectide of the invention may have a use in gene therapy. The PRO polymetide, its agonist, antagonist, or antibody that specifically binds to the copyapptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, inventile chronic arthritis, a spondyloarthropathy, systemic selerosis, and idopathic inflammatory myopathy, Signen's syndrome, systemic sclerosis, autoimmune haemolytic anaemia, autoimmune trombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary disease, infectious or autoimmune chronic active hepatitis, primary continumente or immune-mediated skin disease, a bullous skin disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, asthma, allergic rhintis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, reperingentic presentitivity, urticaria, an immunologic disease, hypersensitivity presensitivity presensitiv
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Pred. No. 0;
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This invention describes a novel polymucleotide and polypeptide sequence for the antigen detected by the antibody MCA 44-3A6. This antigen is designated Labyrinthin (Lab). Antibodies directed to the Labyrinthin and Lab, and Labyrinthin (Lab). Antibodies directed to the Labyrinthin (Lab) protein are useful for the detection of Lab. The Lab protein is useful in diagnostic assays for cancer, e.g. to monitor the presence and amount of antibodies (this method is especially useful for cancer calls that have the Lab marker). As the Lab gene is not tissue-specific, it will detect cancer regardless of which organ it occurs in. Peptides cancer regardless of which cancer. Antibody MCA 44-3A6 is able to differentiate antigens associated with adenocarcinomas. However, the sequence of the antigen detected by this antibody as not been elucidated in the prior art. Determination of the polypeptide and polymucleotide sequence of this antigen would enhance its usefulness in cancer diagnosis, treatment and prevention. The present invention discloses the sequence of the antigen recognized by the MCA 44-3A6 antibody. This sequence concodes the human lab protein described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTGTCGTTTGGTTTGATCTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTAT 281
                                                                                                                 as a diagnostic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Match 27.5%; Score 640; DB 2; Length 24.
Local Similarity 99.9%; Pred. No. 6.5e-287;
Les 690; Conservative 0; Mismatches 1; Indels
                                                                                                           Novel Labyrinthin polynucleotides and polypeptides used marker for cancer and in anticancer vaccines.
                                                                                                                                                       Claim 1; Fig 1; 34pp; English.
           (RADO/) RADOSEVICH J A.
                                                                  WPI; 1999-580307/49.
                                                                                  P-PSDB; AAY33642
                                        Radosevich JA;
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                                                                                                                                   AAATGGTACACGAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCACAG
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                                     645
                                                             821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mcnabb A;
                              GATACAGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAA
                                                                                                                                                                                                                                                                 cDNA encoding clone #48005 (L979P) of lung tumour protein version #2
                                                                                                                                                                                                                                                                                         Lung tumour; cancer; T cell; immune response stimulator; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynuclectide encoding a lung tumor polypeptide useful for stimulating and/or expanding T cells specific for a tumor protein.
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is M, Carter D, Fanger GR, Vedvick TS, Bangur CS,
Fanger N, Switzer A, Mcneill PD, Clapper JD;
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                                                                                                           AATGAAGGGATAGAAATCACAGAAGTAACTG 852
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                                                                                                                                                                                                 ABK39743 standard; cDNA; 2442 BP
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2000US-00651563.
2000US-00651563.
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2000US-00677419.
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Marnerakis M, Carter
A. Fanger N, E
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13-DEC-2000;
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29-AUG-2000;
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DB 6; Length 2442;

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                                                                                                                                           GATGCTGATGGTGATGAGATTTTGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAAA
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                                              222 GCTGTCGTTTGGTTTGATCTTGTTGACTATGAGGAAGTTCTAGGAAACTAGGAATCTAT
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                                162 GGAACTICATICITCACGIGGITIAIGGIGAIIGCATIGCIGGGCGICTGGACAICTGIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lung cancer-associated cDNA L979P extended sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; lung cancer; ss; lung tumour; cytostatic; vaccine; I cell expansion; CD4; CD8.
          Indels
Pred. No. 6.5e-287;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     822 AATGAAGGGATAGAAATCACAGAAGTAACTG 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACA12072 standard; cDNA; 2442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-MAY-2001; 2001US-00849626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
             690; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2002197669-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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401

461

405

581 465 641 761 645 821

521

13-DEC-2000; 2000US-00736457.

(BANG/)

(WANG/

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GCTGTCGTTTGGTTTGATCTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTAT 281
                                                                                                                                                                                                                             CAAGAAGATGGACCCACAGAGAACCACAACAAGAGGGATGATGAGTTTCTTATGGCGACT
                                                                                               GATGCTGATGGAGGATTTTGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAAA
                                                                                                                                                                                                                                                                                             GAGGAGCAGGTTCCTGTGGAGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAA
                                                                                                                                                                                                                                                                                                                                                                                            ATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAA
                                                                                                                                                                                           CAAGAAGATGGACCCACAGGAGAACCACAACAAGAGGATGATGAGTTTTCTTATGGCGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a polynucleotide encoding a lung tumour protein, comprising a sequence selected from any of the 14 sequences mentioned in complement of S1, sequences (S2) mentioned in specification.

CC complement of S1, sequences consisting of at least 20 contiguous residues CC of S1, sequences consisting of at least 20 contiguous residues CC of S1, sequences that hybridise to S1, sequences having 75%, preferably CC of S1, sequences mentioned in the specification a sequence concorded polypeptide (comprising a sequence (S3) selected from any one of the 4 amino acid sequences mentioned in the specification a sequence concorded by the polynucleotide, or sequences having at least 70%, concorded by the polynucleotide, or sequences having at least 70%, concorded by the polynucleotide operably linked to an expression control sequence, a host cell transformed or transfected with the vector, an isolated antibody (or its antigen-binding fragment) that specifically binds to the polynpeptide, detecting the presence of a cancer of a patient, a fusion protein comprising the polypeptide, an orditions, stimulating and/or expanding the polypeptide, and conditions, stimulating and/or expanding to ells specific for a tumour conditions, stimulating and/or expanding to a time sufficient or antigen-presenting cells, under conditions and for a time sufficient conditions, stimulation and/or expansion of T cells) and inhibiting the presenting cells that express the polynucleotide, protein or antigen presenting cells, and thus inhibiting the development of a cancer in a patient with the polynucleotide, protein or antigen composition for stimulating an immune response in a patient, and for the patient. The polynucleotide, protein and sells are useful in a patient (particularly lung cancer in a patient (particularly lung cancer in a patient (particularly lung cancer in a patient (particularly lung cancer) and protein and oligomucleotide is also useful and proteins of the polynucleotide is also polynucleotide is also of tumour ce
                                                                                                                                                                                                                                                                                                                                                                           Novel lung cancer polymuclectide encoding lung cancer protein, useful for detecting the presence of lung cancer in a patient, and in pharmaceutical compositions, e.g. vaccines, for treating lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptides and profession tumour cells. An amplified portion of the polynucleotide is useful for isolating a full-length gene from a suitable library. The present sequence is a cDNA (full length, extended or partial) isolated from a library derived from lung tumour/cancer cells. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO at seqdata.uspto.gov/sequence.html?DocId=20020197669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang A, Wang T, Switzer AP, Mcneill PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.5%; Score 640; DB 8; Length 2442; 99.9%; Pred. No. 6.5e-287; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2442 BP; 781 A; 391 C; 512 G; 758 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5; Page; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al Similarity 99.9
690; Conservative
                                                                                                                                                                                                                               Fanger GR,
                           BANGUR C S.
FANGER G R.
WANG A.
SWITZER A P.
MCNEILL P D.
CLAPPER J D.
                                                                                                                                                                                                                                                                                                        WPI; 2003-352750/33.
P-PSDB; ABU69516.
                                                                                                                                                                                                                               Bangur CS,
Clapper JD;
                                                                                                                           (SWIT/)
(MCNE/)
(CLAP/)
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AGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGAAGAGAGATG 701
                                                            646 GATACAGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAA 705
                                                                                                                                      762 GATACAGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAA
GAIGTAGATGATAGATTTGAGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCAT
                                                                                           TCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGAAGATGAAAGATTGCACCAT
                                                                                                         88.
                                                                                                                                                                                                                                                                                                                                                               Lung cancer; cytostatic; vaccine; gene therapy; cancer; gene;
                                                                                                                                                                                                                                                                                                                                         Lung cancer therapyand diagnosis associated cDNA #1745.
                                                                                                                                                                                      AATGAAGGGATAGAAATCACAGAAGTAACTG 852
                                                                                                                                                                                                   706 AATGAAGGATAGAAATCACAGAAGTAACTG 736.
                                                                                                                                                                                                                                                                    ACA03258 standard; cDNA; 2442 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-00419356
99US-00419356
99US-00466867
99US-00466867
200US-00519642
200UUS-0053077
200UUS-00546559
                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JUL-2001; 2001US-00902941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-OCT-1999;
17-DEC-1999;
30-DEC-1999;
06-MAR-2000;
12-APR-2000;
27-APR-2000;
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Best Loca Matches

ઠે 셤 705

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The invention relates to novel compositions and methods for the therapy and diagnosis of cancer, particularly lung cancer. The compositions comprise one or more lung tumour polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cells that express such polypeptides, and T cells that are specific for cells expressing such polypeptides. The novel compositions have expressing such polypeptides. The novel compositions have used in the creation of a vaccine. The polynucleotides that encode the lung tumour polypeptides can be used in gene therapy to help in the treatment of lung tumours. This polynucleotide sequence represents a treatment of lung tumours. This polynucleotide sequence represents a treatment of lung tumours. This polynucleotide sequence was not shown in the specification. It has been taken from a World Intellectual Property Organization CD ROM supplied with the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 GCTGTCGTTTGGTTTGATCTTGTTGAGGAAGTTCTAGGAAAACTAGGAATCTAT 281
                                                                                                                                                                                                                                                                                                                                                                             lung cancer; tumour; cytostatic; immunostimulant; vaccine; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAACTTCATTCTTCACGTGGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vedvick TS;
                                                      586 TCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCAT
                                     762 GATACAGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptides and encoding polynucleotides, useful for diagnosing, preventing and/or treating lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sleath PR;
Fanger GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 640; DB 10;
Pred. No. 6.5e-287;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kalos MD,
Carter D,
                                                                                                            852
                                                                                                                               706 AATGAAGGGATAGAAATCACAGAAGTAACTG 736
                                                                                                                                                                                                                                                                                                                                              Human lung tumour cDNA clone, SEQ ID No 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; SEQ ID NO 1791; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Watanabe Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Durham M,
                                                                                                                                                                                                                                      2442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-2001; 2001US-00017754
28-MAR-2002; 2002US-00113872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-OCT-2002; 2002WO-US034777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 690; Conservative
                                                                                                                                                                                                                                      ADH47310 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang T,
Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Johnson JC, Retter MV
Bangur CS, Mcnabb A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-468346/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          human; clone; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003037267-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Henderson RA,
                                                                                                                                                                                                                                                                                                              25-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAY-2003
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                                                                                                                                                                                                                                                                              ADH47310;
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                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes an isolated polynucleotide comprising one of 32 sequences, complement or degenerate variants of them. The polynucleotide is useful for preparing a composition e.g. a vaccine or for gene therapy, for treating or inhibiting development of cancer, e.g. lung cancer. This sequence represents a polynucleotide associated with the compositions and methods for the therapy and diagnosis of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTGAGCAGGAAAATCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGAAGAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATGTAGATGATAGATTTGAGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 ggaacticatrcricacgigaritarggigarigcarigcigggcgicrigacarcrigia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 GCTGTCGTTTGGTTTGATCTTGTTGACGAAGTTCTAGGAAAACTAGGAATCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 GATGCTGATGGTGATGATGATGTGATGATGATGCCAAAGTTTTATTAGGACTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAACTTCATTCTTCACGTGGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATGCTGATGGTGATGGAGATTTTGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGCTGAGCCACACACTGAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGGAGCAGGTTCCTGTGGAGGCAGAACCCCCAGAATATCGAAGATGAAGCAAAAGAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGAGCAGGTTCCTGTGGAGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAGAAGATGGACCCACAGGAGAACCACAACAAGAGGATGATGAGTTTTCTTATGGCGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                 New polynucleotide, useful for preparing a composition for treating inhibiting development of cancer, e.g. lung cancer.
                                                                                                                                                                                                                                                Mcnabb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                           Y, Johnson JC, Retter MW;
Vedvick TS, Bangur CS, MC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2442 BP; 781 A; 391 C; 512 G; 758 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 27.5%; Score 640; DB 8; L. Local Similarity 99.9%; Pred. No. 6.5e-287; Pes 690; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                          Example 5; SEQID NO 1791; 82pp; English.
                                                                                                                                                                                                                               Watanabe
Fanger GR,
               05-JUN-2000; 2000US-00589184.
11-JUL-2000; 2000US-0065153.
29-AUG-2000; 2000US-00651563.
08-SEP-2000; 2000US-00658824.
26-SEP-2000; 2000US-00671325.
06-CCT-2000; 2000US-00677419.
30-CCT-2000; 2000US-00702705.
13-DEC-2000; 2000US-00702705.
                                                                                                                                                                                                                                 Wang I
                                                                                                                                                                                                                                                                                     WPI; 2003-328427/31.
                                                                                                                                                                                               (CORI-) CORIXA CORP
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Durham M, Carter
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The invention relates to a novel isolated polynucleotide comprising a sequence chosen from any one of 40 lung tumour polypeptides or its complements, fragments or degenerate variants. The method of the invention has cytostatic applications and may be useful for detecting and treating lung cancer in a patient, as well as for inhibiting the cells isolated from a patient with at least one component chosen from a polypeptide, polynucleotide or antigen presenting cell (APC) of the polypeptide, polypucleotide or antigen presenting cell (APC) of the invention and administering an effective amount of the proliferated T cells to the patient. The current sequence is that of the human lung cancer-related CDNA of the invention. The current sequence is not shown in the specification per se but is available on the USPTO web-site http:seqdata.uspto.gov/sequence.html?DocID=20030211510.
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                                                                                                                                                                                                                                                                                                                                                                                                         Novel polynucleotide encoding lung tumor polypeptides, useful diagnosing, preventing and treating cancer e.g. lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.5%; Score 640; DB 13; Length 2442; 99.9%; Pred. No. 6.5e-287; ative 0; Mismatches 1; Indels 0
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                                                                                                                                                                                                                                                                       Sleath PR;
Fanger GR,
                                                                                                                                                                                                                                                                       Watanabe Y, Kalos MD,
Durham M, Carter D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; SEQ ID NO 1791; 99pp; English.
11-JUL-2000; 2000US-00614124.
29-AUG-2000; 2000US-00651563.
26-SEP-2000; 2000US-00658124.
26-SEP-2000; 2000US-00677419.
30-OCT-2000; 2000US-00677419.
31-DEC-2000; 2000US-00702705.
31-DEC-2000; 2000US-00702705.
31-DEC-2001; 2010US-0094526.
31-DEC-2001; 2010US-0091754.
28-MAR-2002; 2002US-00113872.
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es 690; Conservative
                                                                                                                                                                                                                                                                    Henderson RA, Wang T,
Johnson JC, Retter MW,
Bangur CS, Mcnabb A;
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                                                                                                                                                                                                                                  (CORI-) CORIXA CORP.
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GATGCTGATGGTGATGGAGATTTTGATGTGGATGATGCCAAAGTTTTATTATTAGGACTTAAA
                                                                                                                                ATTCAGTCCCTTCTCCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGAACTTGCAA
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                                                          GATGCTGATGGTGATGGAGATTTTTGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAA
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990S-00419356.
990S-00476300.
2000US-00519642.
2000US-00519642.
2000US-00519642.
2000US-00546259.
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06-MAR-2000; 2
22-MAR-2000; 2
10-APR-2000; 2
27-APR-2000; 2
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15-OCT-1999;
17-DEC-1999;
30-DEC-1999;
06-MAR-2000;
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The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful a marker for breast cancer and in breast cancer therapy. Sequences given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web
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                               GATGTAGATGATAGATTTGAGACCCTGGAACTTGAAGTATCTCATGAAGAAACCGAGCAT
                                                                 AGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGAAGAGATGTG
                                                                                                 AGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGAAGAGATGATG
                                                                                                                                    TCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGGAAGATTGCACCAT
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GATGTAGATGATAGATTTTGAGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCAT
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detecting presence of polypeptide in sample, as a marker for breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
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                                                                                                                                                                                                                                                                                                       AATGAAGGGATAGAATCACAGAAGTAACTG 736
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                                                                                                                                                                                                                                                                                                                                                                                            ACN88788 standard; DNA; 3110
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Length 3110;

26.5%; Score 615; DB 11; I 100.0%; Pred. No. 2.8e-275;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                 TATGGCGACTGATGTAGATGATAGATTTGAGACCCTGGAACCTGAAGTATCTCATGAAGA
                                                                                                                                                                                                                                                                                           895 AACCGAGCATAGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGA
                                                                                                                                                                                                                                                                                                                                           955 AGAGATGATGTCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                             1075 ACCTCTAGAAATGAAGGGATAGAAATCACAGAAGTAACTGCTCCCCCTGAGGATAATCC
                                                                        CACTGAGCCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACCCCCAGAATATCGAAGATGAAGC
                                                                                                                        AAAAGAACAAATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGA
                                                                                                                                                                        TATGGCGACTGATGTAGATGATTTGAGACCCTGGAACCTGAAGTATCTCATGAAGA
                                                                                                                                                                                                                                                                    632 AACCGAGCATAGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGA
                                                                                                                                                                                                                                                                                                                   AGAGATGTCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGAAAG
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                         AGGACTTAAAGAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGGCTGAGCCACA
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 Mismatches
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  Matches
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ACA92448
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Human infant brain cDNA #1130.
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STACHE-CRAIN
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(DICK/) DICKSON M C.
(JONE/) JONES L W.
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(LABA/)
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ACH47067
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modification and maintenance molecules (PWMM), and the polymucleoride

sequences encoding them. A total of 40 PMM polypeptides (designated PMM

1 to PMMM-40) are disclosed. The sequences of the invention are useful

cor diagnosing a condition or disease associated with the expression of

to for diagnosing a condition or disease associated with the expression of

PMM in a subject, preparing a polycloan or monoclonal antibody, and

generating an expression profile of a sample containing the expression of

polymucleorides. The diseases or conditions associated with decreased

corpression or overexpression of PMMM are cell proliferation disorders (

corpression or overexpression of PMMM are cell proliferation disorders (

corpression or overexpression of PMMM are cell disorders, (

dispendence, atherosclerosis), neurological disorders, (

allergies), developmental disorders (e.g. hypothyroidism, Cushing's

syndrome), gastroinfestinal or paithelial disorders, and infections. The

PMMM polypeptides or their fragments are useful in screening compounds

for effectiveness as agonists or antagonists of the polypeptides, or in

caltering the expression of the target polymucleotide and compounds that

corporation or modulate the activity of the polypeptide.

ACA92416-ACA92455 encode the human PWMM polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                   New human protein modification and maintenance molecules (PMMM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMMM expression e.g. cancer, atherosclerosis, or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 GATGCTGATGGTGATGGAGATTTTGATGTGGATGATGCCAAAGTTTTATTAGAGACTTAAA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGCTGAGCCACACACTGAGCCC 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             462 ATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAA 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGTCGTTTGGTTTGATTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTAT 281
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                                                                                                                                                                                     Ramkumar J, Gorvad AE, Baughn MR, Emerling BM, Yang J, Lee SY; Tran UK, Becha SD, Duggan BM, Lee EA, Griffin JA, Li JX; Sprague WW, Hafalia AJA, Chawla MK, Lehr-Mason PM, Kable AE, Yue Marquis JP, Yao MG, Richardeon TW, Tang TY, Jin P, Chien D; Bhatia U, Burrill JD, Lee S, Blake JJ, Ho A, Zheng W;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2648 BP; 844 A; 420 C; 545 G; 839 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 306; 311pp; English.
12-OCT-2001; 2001US-0329689P.
25-OCT-2001; 2001US-0335703P.
09-NOV-2001; 2001US-034887P.
28-NOV-2001; 2001US-0334145P.
06-DEC-2001; 2001US-03317451P.
                                                                                                                                              (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                  Gorvad AE,
                                                                                                                                                                                                                                                                                                          2003-430274/40.
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P-PSDB; ABU92053.
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479 ATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAA 538
                                           CAAGAAGATGGACCCACAGGAGAACCACACAACAAGAGGATGATGAGTTTCTTATGGCGACT
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Human, 88; sequencing by hybridisation, SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.

Ľ, Jones Dickson MC, Stache-Crain B, New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.

Claim 1; SEQ ID NO 34279; 44pp; English.

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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50813, whose sequence was determined by the technique of SBH (sequencing by hybridiaation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleac and sequences care useful in diagnostics as axpressed sequence tags (BST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of procein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The secent sequence cobtained in electronic format directly from USPPTO at cottonic format directly from USPPTO at sequence. Obtained in electronic format directly from USPPTO at sequence.

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Fig 1; 796pp; English.
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Matches 359; Conservative
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                                                                                                                                                                                                                                                                                 CIGAGITIGAAGCGICGCICAGACAGGCAACAATITCIAGGICATAIGAGAGGITCCCIG 1331
                                                                                                                                                                     GTGAATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAGTCCACGAGCAAGATATGGG 1151
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                                                                                                                                                                                                                                                                                            44 TITCCTGTGGAAGAACAGCAGGAAGTACCACCAGAAACAAATAGAAAAAACAGATGATCCA 103
                                                                                                       164 ATTAAAGCTGAACTTGATGCTGCAGAAAACTCCGTAAAAGGGGGAAAATTGAGGAAGCA 223
                                                                                                                                                                                     Grgaargcartrraagaacragracgcaaaracccrcagagrccacgagcaagarafggg 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy.
                                                                                                                                                                                                                                                        AAGGCGCAGTGTGATGATTTTGGCTGAGAAGAGGAAGTAATGAGGTGCTACGTGGA
                                                         ATTAAAGCTGAACTTGATGCTGCAGAAAACTCCGTAAAAGGGGAAAAATTGAGGAAAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Human colon cancer related nucleotide sequence SEQ ID NO:3202.
                      Length 502;
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   BP; 178 A; 97 C; 119 G; 106 T; 0 U; 2 Other;
                                      0; Indels
                                                                                                                                                                                                                                                                                                                      CTTACCCTGCAGAGATTAGTTCAACTATTTCCCAATGAT 1370
                                                                                                                                                                                                                                                                                                                                 CTTACCCTGCAGAGATTAGTTCAACTATTTCCCAATGAT 502
                     19.8%; Score 459; DB 9; 100.0%; Pred. No. 1e-202;
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                                       0; Mismatches
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Thiaglingam A, Lewis ME;
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                                                                                                                                                                                                                                                                                                                                                                                      ABQ59507 standard; cDNA; 660
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                                       Matches 459; Conservative
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                               Similarity
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    Sequence 502
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                      Query Match
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AB056306 to AB060787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78993 to ABB79004 represent proteins encoded by the AB060776 to AB060787 nucleic acid sequences. (I) can be encoded by the AB060776 to AB060787 nucleic acid sequences. (I) can be caded in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I), and for determining the phenotype of cells in a sample of coll cancer in a cell or tissue type, for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate or acorrasponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colon cancer; T cell; tumour protein; C634S; C635S; C637S; C640S; C636S; humoral immune response; cellular immune response; cytostatic; immunostimulant; human; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 660 BP; 131 A; 181 C; 123 G; 221 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.4%; Score 359; DB 6; Le 100.0%; Pred. No. 3.4e-156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colon cancer associated human cDNA sequence #277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08; Pred. ...
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New isolated nucleic acids and polypeptides capable of eliciting humoral and/or cellular immune response, useful for diagnosing, preventing or treating cancer, particularly colon cancer.
                                        Secrist
                                       Lodes MJ,
Stolk JA;
                                       Indirias CY,
, Durham M,
                                                                                      Claim 1; SEQ ID NO 277; 87pp; English.
                                       Xu J, In
Smith CL,
07-FEB-2001; 2001US-0267382P.
11-MAY-2001; 2001US-0290322P.
12-UUJ-2001; 2001US-0305265P.
16-AUG-2001; 2001US-0313077P.
                                      Chenault RA,
Fanger GR,
                                                      WPI; 2003-040540/03.
                           (CORI-) CORIXA CORP.
                                      Jiang Y,
Carter D,
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                                                                                                630 GAAACCGAGCATAGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATG 689
                                                                                                                               GAAACCGAGCATAGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATG 100
                                                                                                                                                                                          281 CCTGTAGAAGATTCACAGGTAATTGTAGAAGTAAGCATTTTTCCTGTGGAAGAACAG 340
                                                                                                                                                                 GAAGAGATGATGTCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGAA 749
                                                                                                                                                                                                                                   750 AGATTGCACCATGATACAGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATAT 809
                                                                                                                                                                                                                                                                                                      810 GAACCTCTAGAAAATGAAGGGATAGAAATCACAGAAGTAACTGCTCCCCCTGAGGATAAT 869
                                                                                                                                                                                                                                                                                                                                                                      CCTGTAGAAGATTCACAGGTAATTGTAGAAGAAGTAAGCATTTTTCCTGTGGAAGAACAG 929
                                                                      Gaps
                                                                    ;
                              10.7%; Score 249; DB 11; Length 495; ilarity 99.7%; Pred. No. 4.9e-105; Conservative 0; Mismatches 1; Indels (
Sequence 495 BP; 183 A; 95 C; 111 G; 104 T; 0 U; 2 Other;
                                               Best Local Similarity
Matches 299; Conserv
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                                  Query Match
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RESULT 20
ACH93769/c
ID ACH93769 standard; DNA; 161 BP.
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(first entry) 29-JUL-2004

Human genome derived single exon probe #26964.

Human; probe; ss; gene expression; single exon probe; microarray;, alternative splicing event; genomic alteration.

Homo sapiens.

US2003194704-A1.

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16-OCT-2003.

03-APR-2002; 2002US-00029386

03-APR-2002; 2002US-00029386

(PENN/) PENN S G. (RANK/) RANK D R. (HANZ/) HANZEL D K.

Penn SG, Rank DR, Hanzel DK;

WPI; 2004-119264/12.

New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues.

Claim 1; SEQ ID NO 26964; 80pp; English.

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide capteness in the specification, or their complements or fragments, and sendences in the specification. The probe is a single exon probe that conding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that conding at least 8 amino acids of any of the 6888 amino acid sequences (bybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially.

Condressable set of single exon nucleic acid probes for measuring human gene expression, a method of probes cited above, where each of the plurality of probes gited above, where each of the plurality of probes gited above, where each of the plurality of probes of the above and addressably isolatable or amplifiable from the single exon microarray for measuring human gene expression, a vector comprising at least 8 method of probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above mentioned amino acid sequences (Optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to thousn gene expression and abscribtion, and a computer-readable storage medium which contains a database having a plurality of records cited above. The probes methods and apparatus are useful in gene expression and addition, the probes methods and apparatus as tools for surveying a pecific exon, or in constructing genome-derived single exon microarrays. The addition, the probes are used in identifying and characterising gross alterations in the genomic lower by the probes are used in identifying and characterising gross alterations in the genomic lower by priming the synthesis of nucleic acids or in expressing the ORF-encoded peptide cite

Sequence 161 BP; 45 A; 49 C; 25 G; 42 T; 0 U; 0 Other;

segdata.uspto.gov/seguence.html?DocID=20030194704

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Claim 4; Page 131; 179pp; English
                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                             임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expression human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human cells or amplifiable from the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of exon microarray for measuring human gene expression, a vector comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid so isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to measure gene expression, a method of mostomer destring to measure gene expression, a method of providing chuman gene expression data by subscription, and a computer-readable secon probe croord including data on the expression of a single exon probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                       110 GGAACTICATICTICAGGGGGTGTTAIGGGGGTGTTGCATIGCTGGACGTCTGGACATCTIGTA 51
                              Gaps
                                                                                                                                                                                                                                                                                                           Human, probe, ss, gene expression, single exon probe, microarray, alternative splicing event, genomic alteration.
                              ..
0
4.5%; Score 104; DB 12; Length 161;
100.0%; Pred. No. 1.4e-37;
ive 0; Mismatches 0; Indels (
                                                                                                           222 GCTGTCGTTTGGTTTGATCTTGTTGACTATGAGGAAGTTCTAGG 265
                                                                                                                          GCTGTCGTTTGGTTTGATCTTGTTGACTATGAGGAAGTTCTAGG 7
                                                                                                                                                                                                                                                                                  Human genome derived single exon probe #13264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15; SEQ ID NO 13264; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rank DR, Hanzel DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-2002; 2002US-00029386.
                                                                                                                                                                                                                                                                                                                                                                                                                                03-APR-2002; 2002US-00029386
                                                                                                                                                                                            069/c
ACH80069 standard; DNA; 592
                                                                                                                                                                                                                                                          (first entry)
                               104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-119264/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 surveying tissues.
                   Similarity
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                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                          29-JUL-2004
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                                                                                                                                                                                                                                  ACH80069;
      Query Match
Best Local
                               Matches
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cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alternative splicing events, in detecting and characterising gross smaller genomic alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 GGAACTICATICITCACGIGGITITAIGGIGAITIGCAITIGCIGGCGICTGGACAICTGIA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; gene therapy; protein therapy; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; autoimmune disease; AIDS; developmental abnormality; foetal deficiency; Alzheimer's disease; cognitive disorder; schizophrenia; immunological disorder; mood disorder; immune deficiency disease; respiratory disorder; arthritis; skeletal; haematopoietic disorder; neural; osteoporosis; metabolic disorders;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 GGAACTTCATTCTTCACGTGGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, immune deficiency diseases or blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiovascular; endocrine; gastrointestinal; asthma; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
4.5%; Score 104; DB 12; Length 592;
Best Local Similarity 100.0%; Pred. No. 1.4e-37;
Matches 104; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 592 BP; 220 A; 122 C; 79 G; 171 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGTCGTTTGGTTTGATCTTGTTGACTATGAGGAAGTTCTAGG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY01148, AAY01190, AAY01191, AAY01192, AAY01193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 GCTGTCGTTTGGTTTGATCTTGTTGACTATGAGGAAGTTCTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein gene 14 clone HAGBZ81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feng P, Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
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97US-0051480P.
97US-0058598P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX22124 standard; DNA; 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US013608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1997;
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12-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JAN-1999
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The invention relates to nucleic acid sequences (AAX22111 to AAX22134) encoding human secreted proteins (AAY01155 to AAY01159). The secreted proteins (AAY01155 to AAY01159). The secreted protein sequences are deposited with the ATCC under deposit number ATCC 209118. Host cells comprising recombinant vectors containing the nucleic acid sequences are used for the recombinant production of the nucleic acid sequences are used for the recombinant production of the number of a secreted proteins. The polymuclectide and amino acid sequences are useful for are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Pathological conditions can be also diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypeptides in a sample or by determining products for the diagnosis or treatment of polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developmental abnormalities and foctal deficiencies, action autoimmune diseases, lymphomas, Alzheimer's and cognitive disorders, actoinmune deficated disorders, immune deficiency disorders, actionated disorders, and action disorders, neural disorders, immune disorders, actionated disorders, osteletal disorders, osteletal disorders, endocrine disorders are also useful for identifying their binding partners. The present sequence represents a number and clone identification)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 AGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAGATTTTGATGTGGATGATGCCAA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; cancer; hyperproliferative disorder; rheumatoid arthritis; autoimmune disorder; haematopoietic disorder; anaemia; allergic reaction; asthma; cardiovascular disorder; wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1382 BP; 413 A; 216 C; 288 G; 464 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Match 3.1%; Score 72; DB 2; Length 138.
Local Similarity 100.0%; Pred. No. 1e-22;
les 72; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vulnerary; cardiant; gene therapy; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA39640 standard; cDNA; 1382 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-2002; 2002WO-US008123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 AGTTTTATTAGG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 AGTTTTATTAGG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2002102993-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 23
셤
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The invention relates to novel genes ADA39629-ADA40565 and proteins
C ADA40566-ADA41501 for human secreted proteins, useful for preventing,
c treating or ameliance in medical conditions e.g. by protein or gene
C therapy. The polypeptides, nucleic acid molecules, antibodies or their
C fragments, and agonists or antagonists that bind to the polypeptide are
C diagnosing or treating a diagnostic or pharmaceutical composition for
C diagnosing or treating cancer or other hyperproliferative disorder. The
C polypeptides and nucleic acid molecules are also useful for detecting,
C preventing, diagnosing, prognosticating, treating or ameliorating cancer
C or other hyperproliferative disorders including neoplasms, autoimmune
C or other hyperproliferative disorders (e.g. anaemia,
C or other hyperproliferation and disorders (e.g. anaemia,
C or other hyperproliferation and disorders (e.g. anaemia,
C or other hyperposia,), alleagic reactions including astemm or excema,
C or other hyperposia, alleagic reactions including astemm or casema,
C or other hyperposia, alleagic reactions including astemm or casema,
C or other disorders (e.g. ischemia-reperfusion injury, inflammatory
C or other disorders (e.g. ischemia-reperfusion injury, inflammatory
C or other disease or Crohn's disease, cardiacion injury, inflammatory
C or other disease or Crohn's disease, or anaemia,
C or other disease or Crohn's disease, or anaemia,
C or other disease or crohner including HIV/AIDS), or wound healing and
C or other inflamone including HIV/AIDS), or wound healing and
C or of epithelial cell proliferation, radiation hybrid markers, or as
C or other disance immunological probes for differential identification
C or this patent did not form part of the private or or disagnostic providing lamunological probes to the private or disagnostic prov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 AGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAGATTTTGATGTGGATGATGCCAA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cardiant, antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antiinflammatory; nootropic; neuroprotective; antiparkinsonian; gene therapy; human; cardiovascular disorder; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                  secreted proteins and nucleic acid molecules, useful for a diagnostic or pharmaceucutical composition for diagnosting or treating cancer or other hyperproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.1%; Score 72; DB 8; Length 1382; Best Local Similarity 100.0%; Pred. No. 1e-22; Matches 72; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1382 BP; 413 A; 216 C; 288 G; 464 T; 0 U; 1 Other;
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                                                                                                                                                                          Claim 9; SEQ ID NO 22; 3205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACC50349 standard; cDNA; 1382 BP.
                                                                                                                           asthma, allergies or AIDS.
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WPI; 2003-175238/17.
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28-NOV-2002.

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multiple sclerosis; ischaemic brain injury; Parkinson's disease;
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                                                               gene,
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                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel human secreted proteins (ABR47633-6 ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences are useful for the preparation of a diagnostic corp pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary carteriosclerosis and myocardial ischaemia), neural disorders, immune system disorders muscular disorders, pulmonary disorders, reproductive disorders; immune cyproliferative disorders and/or cancerous diseases and conditions, for treating thrombosis and arteriosclerosis, for treating or infection, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in neuronal disorders or infection, for the analysis and arteriosclerosis, for treating or neurodegenerative conditions such as Alzhaimer's disease and Parkinson's disease, to enhance bone and periodontal regeneration and aid in tissue tramsplants or bone grafts, to prevent skin aging or hair loss, to stimulate growth and differentiation of haematopoietic cells and bone carnow cells when used in combination with other cytokines, to marrow cells when used in combination or the marrow cells when used in combination or provinces, to maintain or treated to the marrow cells when used or decrease differentiation or provinces, to maintain or treated to the marrow cells when the marrow of decrease differentiation or provinces, to maintain or the marrow c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunosuppressive; antiinflammatory; antiasthmatic; antiallergic; cytostatic; cerebroprotective; neuroprotective; nootropic; cardiovascular; antiatreriosclerotic; gene therapy; human secreted protein; immune disorder; inflammation; respiratory disorder; cancer; CNS disorder; neurodegenerative disorders; inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
                                                                                                                                                                                                                                   Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           embryonic stem cells, or to modulate mammalian characteristics or metabolism. Note: The sequence data for this patent was published in electronic format and is available from WIPO at
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tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene encoding human secreted protein #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.1%; Score 72;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                              Claim 21; SEQ ID NO 16; 1881pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADAS5835 standard; DNA; 1382 BP
                                                                                                                                                                                                                                                                          disorders such as arrhythmia.
                                             21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001UȘ-0331287P.
         19-MAR-2002; 2002WO-US009785
                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-2003 (first entry)
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es 72; Conservative
                                                                                                                                                             Ruben SM;
                                                                                                                                                                                                 WPI; 2003-129429/12
                                                                                                                                                               Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323
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Matches
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The invention relates to 592 new human secreted polypeptides useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, and conditions, respiratory disorders, cancers, CNS disorders, and cancers and cancers are least 95% identical to the new sequences. The polypeptides, antibodies or antibody fragments that bind to the polypeptides, mucleic acids encoding the polypeptides, agonists or antagonists that binds to the polypeptide, are useful in preparing disgnostic or pharmaceutical compositions for diagnosing, treating or preventing an e.g. immune compositions for diagnosing, treating or preventing an e.g. immune compositions for disorders (e.g. gastric, ovarian or lung cancer) CNS disorders (e.g. multiple sclerosis or ischaemic Derain injury), neurodegenerative conspiratory disorders (e.g. parkinson's disease or Alzheimer's disease), and cardiovascular disorders (e.g. atherosclerosis or myocarditis). The cation controlling gene expression through triple helix formation or antisense DNA or RNA, in gene therapy, for identifying individuals from minute biological samples, in forensic biology, and as hybridization or antisense DNA or RNA, in gene therapy, for identifying individuals from minute biological samples, in forensic biology, and as hybridization or antisense DNA or RNA, in gene therapy, for identifying individuals for meating or preventing neural disorders, immune system disorders, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, reproductive, gastrointestinal, pulmonary, cardiovascular, can agene encoding one of the polypeptide of the invention. Note: The sequence data for this patent did form man discense in the polypeptide of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 AGGAAAACTAGGAATCTATGATGCTGATGGAGATTTTGATGTGGATGATGCCAA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human secreted polypeptides and polynucleotides, useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or neurodegenerative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 AGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAGATTTTGATGTGGATGATGCCAA
Alzheimer's diseass, atherosclerosis, myocarditis, chromosome mapping triple helix formation, antisense gene therapy, forensic biology; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 21; SEQ ID NO 24; 1754pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-MAR-2002; 2002WO-US008278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen CA, Ruben SM;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                              WO2002102994-A2
                                                                                                                                                                                                        Homo sapiens.
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293 AGTTTTATTAGG 304

RESULT 26 ABN38322

ABN38322 standard; DNA; 60 BP.

ABN38322;

(first entry) 15-JUL-2002

Human spliced transcript detection oligonucleotide SEQ ID NO:11070.

Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.

Homo sapiens.

WO200210449-A2.

07-FEB-2002.

20-JUL-2001; 2001WO-IB001903.

28-JUL-2000; 2000US-0221607P. 02-MAY-2001; 2001US-0287724P.

(COMP-) COMPUGEN INC.

Mintz E, Mintz L, Faigler S; Shoshan A, Wasserman A,

New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-specific genes. WPI; 2002-257383/30.

Example 1; SEQ ID NO 11070; 47pp; English.

The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcribed from multiple

() transcriptome comprises messenger RNAs transcribed from multiple

() transcription units that populate a genome. The library comprises several configuration units that populate a genome. The library comprises several configuration of the genome, which encodes one or more messenger RNAs splice variants. The configuration of the genome, which encodes one or more messenger RNA splice variants. The configuration of the genome, which encodes one or more messenger RNA splice variants. The configuration of the genome, which encodes one or more messenger RNA splice variants of human or animal transcriptome and splice variants of human or animal transcriptomes. The libraries and splice variants of human or animal transcriptomes. The libraries may also be used as specialised minication of the proposition of the secondary of tissue configuration or pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition, to detect of variants of a transcriptome of a patient suffering from a particular developmental specific pathological condition, to detect of variants of a transcriptome of a patient suffering from a particular configuration. N.B. The sequence data for this patent did not form miss, human and mise, which are used in the exemplification of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_equences

Sequence 60 BP; 22 A; 8 C; 17 G; 13 T; 0 U; 0 Other;

Query Match

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672 GACTGTAATCAGGATATGGAAGAGATGATGTCTGAGCAGGAAAATCCAGATTCCAGTGAA 731 1 GACTGTAATCAGGATATGGAAGAGATGATGTCTGAGCAGGAAAATCCAGATTCCAGTGAA 0; Gaps 2.6%; Score 60; DB 6; Length 60; 100.0%; Pred. No. 4.2e-17; tive 0; Mismatches 0; Indels Local Similarity 100.0 Best Loca Matches

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564/c ADN95564 standard; DNA; 2208 BP. (first entry) 01-JUL-2004 ADN95564; RESULT

Human BEC/LEC-related gene sequence SeqID487.

growth, differentiation, blood endothelial cell; BEC; lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3; lymphatic growth agent; VEGF-C; VEGF-D; antianglogenic; cytostatic; vasotropic; antiinflammatory; gene therapy; endothelial cell disorder; inflammatory disease; cancer metastasis; lymphatic system; gene; ds; human.

Homo sapiens.

WO2003080640-A1.

02-OCT-2003.

07-MAR-2003; 2003WO-US006900.

07-MAR-2002; 2002US-0363019P.

(LUDW-) LUDWIG INST CANCER RES. (LICN) LICENTIA LTD.

Alitalo K, Makinen T,

Petrova T, Saharinen P, Saharinen J;

2003-876899/81. P-PSDB; ADN95563 Example 1; SEQ ID NO 487; 176pp; English.

This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic endothelial cells (LEC) comprises contacting endothelial cells with a composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating bereditary lymphocedema comprises contented with a mutation in at least one allele of a gene encoding a LEC protein, where the mutation in at correlates with lymphocedem and human subjects, and with the provise that the LEC protein is not VEGFR-3; and administering to the subject a correlates with lymphocedem a lymphatic growth agent selected from VEGFC or VEGF Deplypeptides and polymucleotides. The invention may be useful for the development of compounds with an antianglogenic, cytostato, vasorropic or antianflammancery activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells in treating hereditary lymphocedem; in screening for an endothelial cells, in treating hereditary or to bredisposition to the disorder or in monitoring the efficacy or toxicity of or a drug on endothelial cells. The agent is useful in manufacturing a cell or lymphatic vessel endothelial cells growth agent may also be used in manufacturing a medicament for the treatment of hereditary lymphocedem resulting from a mutation in a LEC gene or of other diseases and cancer metestasis via the lymphatic systems agent may also be used in manufacturing a medicament of the treatment of hereditary lymphocedem resulting from a mutation in a LEC gene or of other diseases involving the lymphatic vessels, such as carrious inflammatory diseases and cancer metestasis via the lymphatic system. The present sequence is that of a human LEC/BEC differentially enemended by the present enemended to the method of the invention. Note the sequence does not not annear in the method of the invention. sequence does not appear in the specification but was obtained by th indexer using the source data given in table 14 of the specification

Sequence 2208 BP; 621 A; 428 C; 484 G; 675 T; 0 U; 0 Other;

ö 2.5%; Score 59; DB 11; Length 2208; 100.0%; Pred. No. 1.1e-16; ive 0; Mismatches 0; Indels (Best Local Similarity 100.0 Matches 59; Conservative Query Match

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Gaps

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This invention relates to the novel association of protein sequences (and the genes which encode them) to the NP-kappaB pathway. The invention may be useful for the production of compounds with an antinfinamatory, cytostatic, hepatotropic, virucide, antiarthritic, antinfindmanatory, gastrointestinal-Gen, antiasthmatic, antiarthritic, antinfindmanatic, immunosuppressive or immunomodulator, cerebroprotective, vasotropic, immunosuppressive or immunomodulator, or for gene therapy. The proteins and nucleotides are useful for diagnosing, preventing, treating, or ameliorating conditions or diseases associated with the NP-kappaB pathway. The condition is an immune disorder, an inflammatory disorder, shappaB regulation, cancer, aberrant apoptosis, hepatic disorders, Hoddkin's lymphomas, haematopoietic tumours, hyper-IgM syndromes, hypohidrotic ectodermal dysplasia, ximunodeficiency, viral infections, HIV-1, HTLV-1, ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1, hepatitis B, hepatitis C, EBV, influenza, viral infections, HOV-1, HILV-1,
                                                                                                                                                                                                                                                                                                                                                                                  N. NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide; KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic; antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic; M. antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic; immunosuppressive; vulnerary; gene therapy; immune disorder; Mr. kappaB regulation; cancer; aberrant apoptosis; inflammatory disorder; MF-kappaB regulation; cancer; aberrant apoptosis; Mr. hppatic disorder; MGP-kappaB regulation; cancer; aberrant apoptosis; Mr. Arinked anhidrotic ectodermal dysplasia; Mr. Alinked anhidrotic ectodermal displasia; immunoficiency; Mr. Alinked anhidrotic, inflammatory bowel disease; colitis; asthma; Mr. Alencosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE; autoimmune disorder; hyper immune activity; autoimmune disorder; hyper immune activity; necroic lesion; wound; organ transplant rejection; wound; organ transplant rejection; wound; organ transplant rejection; wound; organ transplant rejection; Mr. HIV propagation; gene; ds; human.
2239 GGCATCCGGAACTGACACCACAGCAGCAGCCTTCCAGCAATTTAGCATGAATTC 2297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway.
                              59 GGCATCCGGAACTGACACCCACGAGGACGCAGCCTTCCAGCATTTAGCATGAATTC
                                                                                                                                                                                                                                                                                                                                            Human NF-kappaB pathway-associated gene SeqID177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carman J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 177; 237pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nadler SG, Neubauer MG, Feder JN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                    ADR14176/c
ID ADR14176 standard; DNA; 2208 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JAN-2004; 2004WO-US000798.
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                                                                                                                                                                                                                                                                                             (first entry)
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P-PSDB; ADR14177.
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                                                                                                                                                                                                                                                                                                21-OCT-2004
                                                                                                                                                                                                                                               ADR14176;
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The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, antithemutatic, immunosuppressive, osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic, antiathmatic, hepatocropic, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
survival, evasion of immune responses, rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick syndrome, stroke, EAB, autoimmune disorders, disorders related to hyper immune activity, disorders related to aberrant acute phase responses, hypercongenital conditions, birth defects, necrotic leaions, wounds, organ transplant rejection, conditions related to organ transplant rejection, disorders related to aberrant signal transduction, proliferating disorders, cancers and HIV propagation in cells infected with other viruses. The present sequence is that of a human gene which is subject to the novel association with the NF-kappaB pathway of the invention.
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                                                                                                                                                                                                                                                                                                                                                                               2239 GGCATCCGGAACTGACACCCACAGAGACGCAGCAGCTTCCAGCAATTTAGCATGAATTC 2297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral nervous system.
                                                                                                                                                                                                                                                                                                                                                                                                            ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood WI;
                                                                                                                                                                                                                                                                                                   DB 13; Length 2208;
1.1e-16;
nes 0; Indels C
                                                                                                                                                                                                                                                              Sequence 2208 BP; 621 A; 428 C; 484 G; 675 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRO polypeptide encoding cDNA SEQ ID NO:247.
                                                                                                                                                                                                                                                                                                         Query Match
2.5%; Score 59; DB
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 59; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Van Lookeren M,
                                                                                                                                                                                                                           was obtained by the indexer from Genbank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 247; 2940pp; English.
                                                                                                                                                                                                                                                                                                       2.5%; Score 59;
.00.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP23153/c
ID ADP23153 standard; cDNA; 2208 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-419628/39.
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juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune cor vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune cor thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, idiopathic demyelinating polyneuropathy, diallain-barre syndrome, a chronic inflammatory demyelinating polyneuropathy, a hepatchiliary disease, infections or autoimmune chronic active hepatitis, primary cirrhosis, granulomatous hepatitis, sclerobathy, whipple's conflammatory bowel disease, gluten-sensitive enteropathy, whipple's disease, exthem anultiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinits, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, contamplic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus.host disease. The present sequence encodes a PRO protein of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2239 GGCATCCGGAACTGACACCACAGCAGCAGCAGCTTCCAGCAATTTAGCATGAATTC 2297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78993 to ABB79004 represent proteins encoded by the ABG60776 to ABG60787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypoptic encoded by (I) is useful for detecting cancer in a patient sample, and for detecting the presence or absence of a polymoclacitie encoded by an uncleic acid which hybridises to (I) in a cell. A probe/primer derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 GGCATCCGGAACTGACACACACAGAGACGCAGCCTTCCAGCAATTTAGCATGAATTC 1
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genetic analysis; diagnostic; antisense therapy; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human colon cancer related nucleotide sequence SEQ ID NO:3266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.5%; Score 59; DB 13; Length 2208; Best Local Similarity 100.0%; Pred. No. 1.1e-16; Matches 59; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2208 BP; 621 A; 428 C; 484 G; 675 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carroll E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABQ59571 standard; cDNA; 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-2000; 2000US-0237271P.
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Thiaglingam A, Lewis ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-426115/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200229086-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the invention.
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from (I) can be used for determining the presence of a nucleic acid which hybridises to (I), and for determining the phenotype of cells in a sample of cells from a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profilling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying an agent that modulates the function of an apoptosis-associated polypeptide, useful for diagnosing or treating e.g. cancer, comparises comparing the binding of the polypeptide to the candidate agent and to a control agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to novel agents that modulates the function of buman apoptosis associated proteins specified within the specification. Specifically, it refers to a method for the identification of target genes whose expression is correlated with an early stage in the regulation of apoptosis. The present invention describes a method of contacting either candidate agents or control agents to the target genes and assessing the difference of binding and inhibitory activity, where the candidate agent is selected from a low molecular weight organic molecule, an antibody or fragment thereof, an antisense oligonucleotide, a small inhibitory dsRNA, or a ribozyme. As such, the compositions and methods are useful for diagnosing and treating diseases or conditions associated with abnormal apoptosis in mammalian tissue, such as cancer, inflammation, autoimmune or neurodegenerative disorders. Accordingly, they exhibit cytostatic, antiinflammatory, immunosuppressive and
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                    2274 CTTCCAGCAATTTAGCATGCAAGTTCAAGCTTGGGAAACTCTGGAGAGA 2324
                                                                                                                                                                                                                                                                                                                                                                               439 CTTCCAGCAATTTAGCATGAATTCATGCAAGCTTGGGAAACTCTGGAGAGA 389
                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88; apoptosis; cancer; inflammation; autoimmune; metrodegenerative disorder; cytostatic; antiinflammatory; immunosuppressive; neuropprotective; gene therapy; PCR; primer; real-time PCR; RT-PCR; CDIPT.
                                                                                                                                                                                                                                                              ch 2.2%; Score 51; DB 6; Length 583; l Similarity 100.0%; Pred. No. 6e-13; 51; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                     Sequence 583 BP; 170 A; 128 C; 126 G; 152 T; 0 U; 7 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reverse quantitative PCR primer to amplify human CDIPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Keating KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Page 289; 304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADR97461 standard; DNA; 27 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-662402/64.
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Best Local S
Matches 51
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Sequence 23 BP; 9 A; 5 C; 8 G; 1 T; 0 U; 0 Other;

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This invention relates to novel agents that modulates the function of human apoptoais-associated proteins specified within the specification. Specifically, it refers to a method for the identification of target genes whose expression is correlated with an early stage in the regulation of apoptosis. The present invention describes a method of contacting either candidate agents or control agents to the target genes contacting either candidate agents or control agents to the target genes and assessing the difference of binding and inhibitory activity, where the candidate agent is selected from a low molecular weight organic molecule, an antibody or fragment thereof, an antisense oligonuclectide, as small inhibitory dSRNA, or a ribozyme. As such, the compositions and methods are useful for diagnosing and treating diseases or conditions associated with abnormal apoptosis in mammalian tissue, such as cancer, inflammation, autoinmune or neurodogenerative disorders. Accordingly, they exhibit cytostatic, antiinflammatory, immunosuppressive and compositivities. These may also be used for drug screening purposes and in gene therapy. This oligonuclectide sequence is a quantitative PCR primer used to amplify a target gene associated with an exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying an agent that modulates the function of an apoptosis-
associated polypeptide, useful for diagnosing or treating e.g. cancer,
comprises comparing the binding of the polypeptide to the candidate agent
and to a control agent.
neuroprotective activities. These may also be used for drug screening purposes and in gene therapy. This oligonucleotide sequence is a quantitative PCR primer used to amplify a target gene associated with apoptosis regulation, given in an exemplification of the invention.
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Forward quantitative PCR primer to amplify human Cathepsin Cl DNA.
                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     se; apoptosis; cancer; inflammation; autoimmune; neurodegenerative disorder; cytostatic; antiinflammatory; immunosuppressive; neuroprotective; gene therapy; PCR; primer; real-time PCR; RT-PCR; Cathepsin Cl.
                                                                                                                                        Score 27; DB 13; Length 27;
Pred. No. 0.096;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seera L;
                                                                                                       Seguence 27 BP; 10 A; 11 C; 1 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayes I,
                                                                                                                                  1.2%; Sco...
100.0%; Pred. No. v...
0; Mismatches
                                                                                                                                                                                                                          CTGATGGTGATGGAGATTTTGATGTGG 312
                                                                                                                                                                                                                                                                CTGATGGTGAGATTTTTGATGTGG 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Page 289; 304pp; English.
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                                                                                                                                                                                                                                                                                                                                                                 ADR97432 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                   1 Similarity 100.
27; Conservative
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                                                                                                                                                                                                                                                       Drosophila, developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                              Drosophila melanogaster genomic polynucleotide SEQ ID NO 29182.
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     Length 23;
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'--o 0; Mismatches
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Mismatches
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11-JUL-2000; 2000US-00614150.
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                                  23; Conservative
                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and influencial interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB70202). The sequence data for this parent did not form part of the princed specification, but was obtained in electronic form part of the from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                              detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 22853; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                           Li PWD, Myers EW;
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             23-MAR-2001; 2001WO-US009231.
                                                                    23-MAR-2000; 2000US-0191637P.
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11-JUL-2000; 2000US-00614150
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genes from Drosophila and
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llarity 100.0%; Pred. No. 18;
Conservative 0; Mismatches 0; Indels
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ABL19239;
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                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16180-ABL1675) and the encoded proteins (ABBS7071-ABR2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                     0.9%; Score 22; DB 4; Length 2855;
100.0%; Pred. No. 18;
           Claim 1; SEQ ID NO 29179; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL23387 standard; DNA; 3705 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                Gaps
                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                     Drosophila melanogaster genomic polynucleotide SEQ ID NO 9187.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3933;
    Length 3705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 9187; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                ò.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 22; DB 4;
Pred. No. 18;
        4
0.9%; bccd. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%;
    DB (
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                                                                                     276 AGCAGCGGCAACAGCAGCAGCA 297
                                                           57
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100.0%; rx,
0;
                                                             36 AGCAGCGGCAACAGCAGCAGCA
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                          ABL19238 standard; DNA; 3933
                                                                                                                                                                                                                (first entry)
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Best Local Similarity 100.
Matches 22; Conservative
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                                Conservative
                                                                                                                                                                                                                                                                                pharmaceutical; gene; ds
                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-656860/75.
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                     Local Similarity
nes 22; Conserv
                                                                                                                                                                                                                                                                                                                                     WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter JC,
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                                                                                                                                                                                     ABL19238;
         Query Match
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ABL09456
ID ABL094
XX
AC ABL09
                        Best Loc
Matches
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26-MAR-2002

27-SEP-2001.

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABL30212). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic form part of from MIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense GMPR2 siRNA oligomer to knockout apoptosis related gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    se; DNA/RNA hybrid; apoptosis; cancer; inflammation; autoimmune;
neurodegenerative disorder; cytostatic; antiinflammatory;
immunosuppressive; neuroprotective; gene therapy; siRNa; GMPR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5903 BP; 1547 A; 1491 C; 1506 G; 1359 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 21631; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 5903;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.9%; Score 22; DB 4
100.0%; Pred. No. 17;
cive 0; Mismatches
                                                                                                                                            Li PWD, Myers EW;
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  23-MAR-2001; 2001WO-US009231.
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ADR97567 standard; RNA; 21 BP
                                     23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAR-2004; 2004WO-GB000957.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 100.
22; Conservative
                                                                                                                                            Venter JC, Adams M,
                                                                                                                                                                                    WPI; 2001-656860/75.
                                                                                                  (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                    interactions.
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misc_feature
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Synthetic.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more sense from brosophila and for elucidating cell signaling and cell-cell interactions.
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                                              Drosophila melanogaster expressed polynucleotide SEQ ID NO 22850.
                                                                                         developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.9%; Score 22; DB 4; Length 3974; ilarity 100.0%; Pred. No. 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 22850; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               Myers EW;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Li PWD,
                                                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US009231.
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11-JUL-2000; 2000US-00614150.
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         (first entry)
                                                                                      Drosophila; developmental
pharmaceutical; gene; ss.
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                                                                                                                                                 Drosophila melanogaster.
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P-PSDB; ABB65353.
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Best Local Similarity
Matches 22; Conservat
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WO200171042-A2.

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27-SEP-2001

26-MAR-2002

ABL23386;

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Gaps

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New antisense oligonucleotides, useful for treatment and prevention of hypertenaton and myocardial ischemia, are directed against mRNA encoding the betal-adrenoceptor. (UYFL) UNIV FLORIDA. WPI; 2000-271424/23. WO200015783-A2 Phillips MI, 14-SEP-1999; 14-SEP-1998; 19-JUN-2000 23-MAR-2000 AAZ98400; Query Match Matches RESULT 42 AAZ98400 PART SERVICE S ò 셤

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This invention relates to novel agents that modulates the function of human apoptosis-associated proteins specified within the specification. Specifically, it refers to a method for the identification of target genes whose expression is correlated with an early stage in the regulation of apoptosis. The present invention describes a method of contacting either candidate agents or control agents to the target genes contacting either candidate agent of no molecular weight organic molecule, an antibody or fragment thereof, an antisense oligonucleotide, a small inhibitory daRNA, or a ribozyme. As such, the compositions and methods are useful for diagnosing and treating diseases or conditions associated with abnormal apoptosis in mammalian tissue, such as cancer, inflammation, autoimmune or neurodegenerative disorders. Accordingly, they exhibit cytostatic, antiinflammatory, immunosuppressive and neuroprotective activities. These may also be used for drug screening purposes and in gene therapy. This oligonucleotide sequence is an siRNA oligo used to knockout expression of a human gene identified to be associated with the regulation of a human gene identified to be
                                                                             Identifying an agent that modulates the function of an apoptosis-associated polypeptide, useful for diagnosing or treating e.g. cancer, comprises comparing the binding of the polypeptide to the candidate agent and to a control agent.
                                                                                                                                                                                                                                                                                                                                                                                       Example 5; Page 293; 304pp; English.
WPI; 2004-662402/64.
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11-JUL-2001; 2001WO-US021759.
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                                                                                                                                                                                               Dog betal-adrenoceptor gene.
                                                                                                                                                                  21-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYFL ) UNIV FLORIDA.
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                                                                                                                                                                                                                                                                                     Canis familiaris.
                                                                                                                                                                                                                                                                                                                     WO200204623-A2.
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                                                                                                                                                                                                                                                                                                                                                  17-JAN-2002
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23
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                                                                         RESULT 43
                                                                                         ABK40732
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                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Betal-adrenoceptor; antisense; transcription; hypertension; canine; myocardial ischemia; hypotensive; vasotropic; ds.
                                                                                                                         ;
                                                                                           Score 21; DB 13; Length 21; Pred. No. 60;
                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                     Canine betal-adrenoceptor polynucleotide sequence.
                                                              Sequence 21 BP; 4 A; 5 C; 3 G; 2 T; 7 U; 0 Other;
                                                                                                                           Mismatches
                                                                                                                                                          1787 AAACTGGAAGTTAATCCGAGA 1807
                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                AAZ98400 standard; DNA; 1845 BP
                                                                                             0.9%;
100.0%;
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                                                                                                                             Conservative
                                                                                                         Local Similarity
nes 21; Conserv
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The invention provides a composition comprising at least one oligonucleotide, of 9-35 bases, that binds specifically to part of the oligonucleotide, of 9-35 bases, that binds specifically to part of the mRNA, expressed from the gene encoding a mammalian betal-adrenoceptor propertie. Binding of the oligo to the betal-adrenoceptor mRNA alters transcription of the mRNA in cells. The compositions are used to treat diseases associated with increased number or activity of the betal-adrenoceptor polypeptide, specifically hypertension and myocardial ischemia. The compositions can also be used to produce recombinant ischemia. The antisense oligos may also be used to detect the mRNA or related DNA, including visualization within a cell, to generate transgenic animals with altered betal-adrenoceptor activity, and to screen patients for susceptibility to hypertension, by detection of particular alleles of betal-adrenoceptor genes. The present sequence represents the polymuclectide sequence of the canine betal-adrenoceptor (GenBank Acon No: U73207)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel antisense oligonucleotides that specifically bind to mRNA encoding beta 1-adrenoreceptor polypeptide, useful for treating cardiac dysfunction, hypertension, hypertrophy and other cardiovascular diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated antisense oligonucleotide of 9-35 nucleotides in length, which specifically binds to a portion of an mRNA expressed from a gene encoding a mammalian betal-adrenoceptor (AR) polypeptide and alters the translation of the mRNA into the betal-AR polypeptide in a host cell expressing the mRNA. Also included are a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ds; antisense; betal adrenoceptor; betal-AR; vasotropic; hypotensive; cardiant; hypertension; hypertrophy; cardiac ischaemia; cardiovascular disease; cardiac dysfunction; gene.
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 1845;
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53;
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100.0%; Pred. No. 2.,
0; Mismatches
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           Example 4; Page 90-91; 144pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGCAGCGGCTCCGGCAGCGG 73
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nes 21; Conservative
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Matches
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cell comprising the antisense oligonuclectide, and a host cell comprising the vector. A composition comprising the antisense oligonuclectides is useful in the manufacture of a medicament for use in treating or ameliorating hypertension, hypertrophy and cardiac ischaemia in a manumal. A composition comprising the antisense oligonuclectides is also useful for reducing the level of betal-AR polypeptide, the transcription of betal-AR polypeptide specific mRNA in a mammalian host cell, particularly human cell, and for decreasing blood pressure in a promoter capable of expressing the oligonuclectide is operably linked to a promoter capable of expressing the oligonuclectide in the cell. A promoter capable of expressing the oligonuclectide such comprises composition comprising a selected nucleic acid segment that comprises plumiclectide operatively linked to a promoter capable of expressing the collynuclectide in a cell is also useful for reducing the level of beta_l-collynuclectide in a cell is also useful for reducing the level of beta_l-collynuclectide is also useful for cher cardiavacturar diseases and cardiac dysfunction in humans. The present sequence is a mammalian betal-capable in a cell is also useful for antisense colligonuclectide is a mammalian betal-capable of expression in humans. The present sequence is a mammalian betal-capable in a cell is also useful for antisense oligonuclectides of the antisense oligonuclectides of the cardiac dysfunction in humans. The present sequence is a mammalian betal-capable in the mRNA for which is a target for antisense oligonuclectides of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signalling lymphocyte activation molecule; SLAM; SLAM associated protein; SAP; BAT-2; antigen-specific T cell activation; X-linked prollferative disease; XLP; tuberculosis; AIDS; schistosomiasis; cancer; breast cancer; prostate cancer; leukemia; leprosy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New signaling lymphocyte activation molecule associated protein useful in the treatment of tuberculosis and AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents part of a signalling lymphocyte activation molecule (SiAM) associated protein (SAP) gene. A SAP family member polypeptide (such as EAT-2) or a fragment, mutant or fusion can be used for treating a disease involving aberrant SH2 domain-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA sequence of the 5' region/exon 1/intron 1 of murine SAP gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1845 BP; 197 A; 754 C; 647 G; 246 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 15; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 CAGCAGCGCTCCGGCAGCGG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 CAGCAGCGGCTCCGGCAGCGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX60124 standard; cDNA; 4011 BP.
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98US-0099160P.
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                                                                                                                                                                                                                                                                                                                                                                                                     AR gene, L...
the invention
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The present sequence represents an antisense oligonucleotide which inhibits human aspartyl (apparaginyl) beta-hydroxylase (HAAH) gene.

Epidermal growth factor (EGF)-like domains of polypeptides are bydroxylated by HAAH enzymes. HAAH is used in the method of the invention. The specification describes a method for diagnosing a malignant neoplasm in a mammal. The method comprises contacting a body fluid with an antibody which binds to HAAH polypeptide under complex method is useful for diagnosing and prognosing a malignant neoplasm in a bodily fluid e.g. central nervous system (CSS) derived body fluid, blood, serum, urine, saliva, sputum, lung effusion, and ascites fluid of mammal, where the neoplasm is derived from endodermal tissue and is selected from colon canner, breast cancer, paracreatic cancer, liver cancer, cancer of bile ducts, and cancer of the CNS. HAAH antibodies, linked to a cytotoxic agent, are useful for killing tumour cells
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                                                                                                                                        used for
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        Upregulation of SAP
protein-mediated signal transduction in a patient. Upregulation of SAPE family members can be used for the treatment of diseases involving insufficient antigen specific T cell activation (e.g. X-linked prolliferative disease (XLP), tuberculosis, AIDS, schistosomiasis) or cancer (e.g. breast cancer, leukemia), or leprosy Downregulation of SAP family members can be used for the treatment of activation (e.g. autoimmune diseases). The products can also be used featertion and diagnosis
                                                                                                                                                                                                                                                                       Gaps
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human asparyt) beta-hydroxylass; HAAH; malignant neoplasm; tumour;
antisense oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human aspartyl (asparaginyl) beta-hydroxylase antisense molecule.
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                                                                                                                                                                                         Sequence 4011 BP; 1125 A; 828 C; 885 G; 1173 T; 0 U; 0 Other;
                                                                                                                                                                                                                              Score 21; DB 2; Length 4011;
Pred. No. 51;
                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                  3157 GCAGCGGCAACAGCAGCA 3177
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                                                                                                                                                                                                                                                                                                     37 GCAGCGCAACAGCAGCA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Page 57; 76pp; English.
                                                                                                                                                                                                                            Query Match

Best Local Similarity 100.0%; Pr
Matches 21; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF89814 standard; DNA; 20 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF89814;
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Matches
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AAF89814/c
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Diagnosing malignant neoplasm in a mammal, involves contacting mammalia sample with antibody that binds to human aspartyl beta-hydroxylase polypeptide to form antigen-antibody complex and detecting the complex.
                                                                                                                                                                                              Epidermal growth factor-like domain; EGF-like domain; cancer; human aspartyl beta-hydroxylase; HAAH; malignant neoplasm; tumour; antisense oligonucleotide; ss.
                                                                                                                                                                   Human aspartyl (asparaginyl) beta-hydroxylase antisense molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RHOD-) RHODE ISLAND HOSPITAL LIFESPAN PARTNER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; Page 57; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  08-NOV-2000; 2000WO-US030738.
                                                     AAF89812 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-329171/34.
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                                                                                                                                    23-JUL-2001
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                                                                                               AAF89812;
                  RESULT 47
AAF89812/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a cancer, breast cancer, pancreatic cancer, liver cancer, cancer of ducts, and cancer of the CNS. HAAH antibodies, linked to a cytotoxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosing malignant neoplasm in a mammal, involves contacting mammalian sample with antibody that binds to human aspartyl beta-hydroxylase polypeptide to form antigen-antibody complex and detecting the complex.
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                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                               Human aspartyl (asparaginyl) beta-hydroxylase antisense molecule.
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0.9%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
                                       Length 20;
                                                                              0; Indels
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Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 U; 0 Other;
                                     0.9%; Score 20; DB 4; Le
100.0%; Pred. No. 1.7e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carlson RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RHOD-) RHODE ISLAND HOSPITAL LIFESPAN PARTNER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 15; Page 57; 76pp; English.
                                                                                                                          1 CGGACCGTGCAATGGCCCAG 20
                                                                                                                                                   20 CGGACCGTGCAATGGCCCAG 1
                                                                                                                                                                                                                                                                 AAF89813 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-00436184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-NOV-2000; 2000WO-US030738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De La Monte SM,
                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-329171/34.
                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200135102-A2.
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                                                                                     20;
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                                             Query Match
                                                                    Local
                                                                                       Matches
                                                                                                                                                                                                                              RESULT 46
AAF89813/
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contacting mammalian

Carlson RI;

99US-00436184.

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The present sequence represents an antisense oligonucleotide which inhibits human aspartyl (asparaginyl) beta-hydroxylase (HAAH) gene. Epidermal growth factor (EGF)-like domains of polypeptides are hydroxylated by HAAH enzymes. HAAH is used in the method of the invention. The specification describes a method for diagnosing a malgmant neoplasm in a mammal. The method comprises contacting a body fluid with an antibody which binds to HAAH polypeptide under complex forming conditions, and detecting the antigen-antibody complex. The method is useful for diagnosing and prognosing a malignant neoplasm in a bodily fluid e.g. central nervous system (CNS)-derived body fluid, blood, serum, urine, saliva, sputum, lung effusion, and ascites fluid of mammal, where the neoplasm is derived from endodermal tissue and is selected from
                                                                                                                                                                                                                                                                                                                                                                                         colon cancer, breast cancer, pancreatic cancer, liver cancer, cancer of bile ducts, and cancer of the CNS. HAAH antibodies, linked to a cytotoxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.0%; Pred. No. 1.7 tes 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          agent, are useful for killing tumour cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human HAAH antisense oligonucleotide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 AATGGCCCAGCGTAAGAATG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 AATGGCCCAGCGTAAGAATG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABS57871/c
ID ABS57871 standard; DNA; 20 BP.
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CGTGCAATGGCCCAGCGTAA 25

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ch 0.9%; Score 20; DB 8; Length 20; Similarity 100.0%; Pred. No. 1.78+02; 20; Conservative 0; Mismatches 0; Indels Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 U; 0 Other; Local Best Loca Matches

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Gaps

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Human, 88; aspartyl (asparaginyl) beta-hydoxylase; HAAH; antisense; cytostatic; immunostimulant; antibody; neoplasm; tumour; FB50; 86A; 5C7; 19B; brain tumour; aglioma; glioblastoma; astrocytoma; haemangioma; pancreatic carcinoma; colon cancer; breast cancer; pancreatic cancer; liver cancer; c metastatic CNS neoplasm

Homo sapiens.

US2002110559-A1.

15-AUG-2002.

17-MAY-2001; 2001US-00859604.

99US-00436184. 08-NOV-1999;

(WAND/) WANDS J R. (DMON/) DE LA MONTE S M.

(DEUT/) DEUTCH A H. (GHAN/) GHANBARI H A.

Deutch AH, Ghanbari HA; Wands JR, De La Monte SM,

WPI; 2003-066676/06.

Diagnosing neoplasm and inhibiting tumor growth, by contacting tissue of mammal with detectably-labeled antibody which binds to human aspartyl (asparaginyl) beta-hydroxylase.

Example 6; Page 18; 34pp; English.

The invention relates to diagnosing a neoplasm and inhibiting tumour of growth in a wammal, using an antibody that binds to human aspartyl caparaginyl beter bydroxylase (HAAH). Diagnosing a neoplasm comprises contacting a tissue with a detectably-labelled antibody where an increase in level of antibody binding at tissue site compared to the level of increase of binding to normal non-neoplastic tissue indicates the presence of a comparation of antibody binding at tissue site compared to the level of binding to normal non-neoplastic tissue indicates the presence of a daministering the antibody conjugated to a cytotoxic agent to a mammal. Also included are a method of conferring an immune response to a tumour captories fite immune response in a mammal, by administering to the mammal that polypeptide (or a polynucleotide composition encoding the extracellular domain and lacking a cytoplasmic domain of HAAH; omprising an extracellular domain and lacking a cytoplasmic domain of HAAH; which lacks enzymatic attibody or its fragment which binds to HAAH (where the antibody is FB50, FBA, SC7 or 198), a hybridoma cell line chosen from hybridoma FB50, attibody or its fragment which binds to HAAH (where the antibody is FB50, EBA, SC7 or 198), a hybridoma cell line chosen from hybridoma FB50, actor (EGS)-like domain. The methods are useful for diagnosing neoplasm or nemanal, inhibiting tumour growth in a mammal, inhibiting tumour growth in a mammal, inhibiting tumour cell (e.g. glinoma, glioblastoma, astrocytoma or nemanal, inhibiting tumour growth in a mammal inhibiting tumour cell for diagnosing malignant complasms derived from endodermal tissue, e.g. colon cancer, breast compense in a mammal. The method is useful for diagnosing malignant (RNS) e.g. primary malignant CNS eneoplasms of central nervous system (CNS) e.g. primary malignant CNS neoplasms of central nervous system cell or sign and method is also useful for diagnosing neoplasms of central nervous system cell origin and method is also central order of primary and g (CNS) e.g. primary malignant CNS neoplasms of both neuronal and gli cell origin and metastatic CNS neoplasms, and for disgnosing brain tumours e.g. glioma, glioblastoma, astrocytoma or haemangioma. The present sequence represents a Human HAAH antisense oligonucleotide

20 CGGACCGTGCAATGGCCCAG 1

ABS57870,

'870/c ABS57870 standard; DNA; 20 BP.

ABS57870;

(first entry) 06-FEB-2003 Human HAAH antisense oligonucleotide #2.

Human; 98; aspartyl (asparaginyl) beta-hydoxylase; HAAH; antisense; cytostatic; immunosthulant; antibody; neoplasm; tumnour; FBEO; 96A; 5C7; 19B; brain tumnour; glioma; glioblastoma; astrocytoma; haemangioma; pancreatic carcinoma; colon cancer; breast cancer; pancreatic cancer; liver cancer; cancer of the bile ducte; primary malignant CNS neoplasm; mecastatic CNS neoplasm;

Homo sapiens.

JS2002110559-A1.

15-AUG-2002.

17-MAY-2001; 2001US-00859604.

99US-00436184. 38-NOV-1999;

(WAND/) WANDS J R. (DMON/) DE LA MONTE S M. (DEUT/) DEUTCH A H. (GHAN/) GHANBARI H A.

Deutch AH, Ghanbari HA; Wands JR, De La Monte SM,

WPI; 2003-066676/06,

ō Diagnosing neoplasm and inhibiting tumor growth, by contacting tissue mammal with detectably-labeled antibody which binds to human aspartyl (asparaginyl) beta-hydroxylase.

Example 6; Page 18; 34pp; English.

The invention relates to diagnosing a neoplasm and inhibiting tumour of growth in a mammal, using an antibody that binds to human aspartyl (asparaginyl) beca-hydroxylase (HAAH). Diagnosing a neoplasm comprises contacting a tissue with a detectably-labelled antibody where an increase in level of antibody binding at tissue site compared to the level of binding to normal non-neoplastic tissue indicates the presence of a contacting the antibody binding at tissue site. Inhibiting tumour growth in mammal involves administering the antibody conjugated to a cytotoxic agent to a mammal. Also included are a method of conferring an immune response to a tumour cell in a mammal, by administering the antibody, a method of inducing an HAAH polypeptide (or a polymucleotide composition encoding the antibody or its degenerate variant), a fragment of HAAH comprising an extracellular domain and lacking a cytoplasmic domain of HAAH, an antibody or its fragment which binds to HAAH (where the antibody is FB50, 684, 557 or 198), a hybridoma cell line chosen from hybridoma FB50, HA386A, HA35CA and HAA189, and a fragment of HAAH (where the antibody is FB50, 685, 557 or 198), a hybridoma cell line chosen from hybridoma relectively or alpha-ketcoglutarate binding domain and epidermal growth factor (EGF)-like domain. The methods are useful for diagnosing neoplasm correction a mammal, for conferring immune response to a pencratic carcinoma cell and for inducing a HAAH-specific immune response in a mammal. The method is useful for diagnosing malignant concert, pancreatic cancer, liver cancer and cancer of the bile ducts. The method is also useful for diagnosing neoplasms of central nervous system concer, pancreating cancer, liver cancer and cancer of the bile ducts. The method is also useful for diagnosing neoplasms of central nervous system (CNS) e.g. primary malignant CNS neoplasms of central nervous system concer, pancreatic cancer, liver cancer and cancer of the bile ducts.

1 CGGACCGTGCAATGGCCCAG 20

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                                                                                                                                                                                                                                                                                                                                   Human, 88; aspartyl (asparaginyl) beta-hydoxylase; HAAH; antisense; cytostatic; immunostimulant; antibody; neoplasm; tumour; FBBG; 86A; 5C7; 19B; brain tumour; glioma; glioblastoma; astrocytoma; haemangioma; pancreatic carcinoma; colon cancer; breast cancer; pancreatic cancer; liver cancer; cancer of the bile ducts; primary malignant CNS neoplasm; metastatic CNS neoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          οĘ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing neoplasm and inhibiting tumor growth, by contacting tissue mammal with detectably-labeled antibody which binds to human aspartyl (asparaginyl) beta-hydroxylase.
                                                                                                           Gaps
cell origin and metastatic CNS neoplasms, and for diagnosing brain tumours e.g. glioma, glioblastoma, astrocytoma or haemangioma. The present sequence represents a Human HAAH antisense oligonucleotide
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                                                                             Score 20; DB 8; Length 20;
Pred. No. 1.7e+02;
                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ghanbari HA;
                                                     Seguence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                          Local Similarity 100.0%; Pred. No. 1.7 nes 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                              Human HAAH antisense oligonucleotide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deutch AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 6; Page 18; 34pp; English.
                                                                                                                                      6 CGTGCAATGGCCCAGCGTAA 25
                                                                                                                                                    CGTGCAATGGCCCAGCGTAA 1
                                                                                                                                                                                                                        869/c
ABS57869 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-2001; 2001US-00859604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-00436184.
                                                                                   0.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De La Monte SM,
                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (WAND/) WANDS J R.
(DMON/) DE LA MONTE S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEUT/) DEUTCH A H.
GHAN/) GHANBARI H A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-066676/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2002110559-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-NOV-1999;
                                                                                                                                                                                                                                                                                      06-FEB-2003
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                                                                                                                                                                                                                                                            ABS57869;
                                                                                                                                                                  20
                                                                                Query Match
                                                                                                              Matches
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activity or alpha-ketoglurante binding domain and epidermal growth
factor (EGF)-like domain. The methods are useful for diagnosing neoplasm
factor (EGF)-like domain. The methods are useful for diagnosing neoplasm
in a mammal, inhibiting tumour growth in a mammal, conferring an immune
response to a brain tumour cell (e.g. glioma, glioblastoma, astrocytoma
or haemangioma) in a mammal, for conferring immune response to a
pancreatic carcinoma cell and for inducing a HAAH-specific immune
response in a mammal. The method is useful for diagnosing malignant
cancer, pancreatic cancer, liver cancer and cancer of the bile ducts. The
method is also useful for diagnosing neoplasms of central nervous system
(CNS) e.g. primary malignant CNS neoplasms of both neuronal and glial
cell origin and metastatic CNS neoplasms, and for diagnosing brain
tumours e.g. glioma, glioblastoma, astrocytoma or haemangioma. The
tumours e.g. glioma, glioblastoma, astrocytoma or haemangioma. The
tumours e.g. glioma, glioblastoma, astrocytoma or haemangioma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying an agent that modulates the function of an apoptosis-associated polypeptide, useful for diagnosing or treating e.g. cancer, comprises comparing the binding of the polypeptide to the candidate agent and to a control agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/note= "Oligo dT bases added to the 3' end to stabilise
binding"
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HA386A, HA15CA and HA219B, and a fragment of HAAH which lacks enzymatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ss; DNA/RNA hybrid; apoptosis; cancer; inflammation; autoimmune; neurodegenerative disorder; cytostatic; antiinflammatory; immunosuppressive; neuroprotective; gene therapy; siRNA; PPlA.
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1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.0%; Pred. No. 1.7 tes 20; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 AATGGCCCAGCGTAAGAATG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 AATGGCCCAGCGTAAGAATG 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADR97507 standard; RNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Specifically, it refers to a method for the identification of target genes whose expression is correlated with an early stage in the regulation of apoptosis. The present invention describes a method of contacting either candidate agents or control agents to the target genes and assessing the difference of binding and inhibitory activity, where the candidate agent is selected from a low molecular weight organic molecule, an antibody or fragment thereof, an antisense oligonucleotide, a small inhibitory dispray, or a ribozyme. As such, the compositions and methods are useful for diagnosing and treating diseases or conditions and associated with abnormal apoptosis in mammalian tissue, such as cancer, inflammation, autoimmune or neurodegenerative disorders. Accordingly, neuroprotective activities. These may also be used for drug screening organical and in gene therapy. This oligonucleotide sequence is an siRNA cassociated with the regulation of a human gene identified to be associated with the regulation of apoptosis, given in an exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
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0
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Pred. No. 1.7e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 7 A; 3 C; 5 G; 2 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome derived single exon probe #9144.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1789 ACTGGAAGTTAATCCGAGAT 1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ACUGGAAGUUAAUCCGAGAT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 80.0 tes 16; Conservative
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-119264/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the invention.
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Matches
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cc expressed in human cells or tissues. Also included are a spatially-
caddressable set of single exon nucleic acid probes for measuring human

CC gene expression (comprising a plurality of single exon nucleic acid

probes cited above, where each of the plurality of probes is separately

and addressably isolatable or amplifiable from the plurality), a single

condition amino acids of any of the above- method of a single exon

contiguous amino acids of any of the above- mentioned amino acid

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant expression vector; transcription regulatory element;
Klebsiella pneumoniae protein; antibacterial; Vaccine; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 550;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.9%; Score 20; DB 12;
100.0%; Pred. No. 1.6e+02
ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1256 TGCAGACCTGCTGAAGCTGA 1275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-895346/82.
P-PSDB; ABO62587.
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Best Local Similarity
Matches 20; Conserv
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ACH96138/c
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                     The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This sequence encodes a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stably transformed cells expressing endorphin, enkephalin and catecholamine - and artificial organs contg. them, useful for control of pain, esp. implanted in the CNS.
                                                                                                                    Gaps
                                                                                                                                                                                                                                                       Analgesic; pain; bioartificial organ; pro-opiomelanocotin; POMC;
beta-endorphin; CNTF; IgSP-hPOMC; ss.
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                                                                                                    Score 20; DB 11; Length 786;
Pred. No. 1.6e+02;
                                                                                    Sequence 786 BP; 129 A; 220 C; 235 G; 202 T; 0 U; 0 Other;
                                                                                                                   0; Indels
                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 1.0.
Matches 20; Conservative 0; Mismatches
         Disclosure; SEQ ID NO 1933; 932pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          "hPOMC region"
                                                                                                                                                                                                                                                                                                                                                     "IgSP region"
                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                    294 chaccachachachachach 275
                                                                                                                                     38 CAGCGGCAACAGCAGCAGCA 57
                                                                                                                                                                                           AAT62523 standard; DNA; 849 BP
                                                                                                                                                                                                                                        IgsP-hPOMC fusion DNA sequence
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/product=
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43. .186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wong S;
                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
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                                                                                                                                                                                                                                                                                                                                    misc_feature
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                                                                                                                                                                                                           AAT62523;
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                                                                                                                                                                                                                                                                                                                      5'UTR
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                                                                                                                                                                             RESULT 54
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                                   A DNA sequence (AATG2523) comprising a fusion between IgSP and human proposiomelanocortin (POMC) DNA can be utilised in the construction of vectors for the expression of endorphin apds. Cleavage enzymes present in host cells can generate a suite of endorphins from POMC, some or all of which have analgesic properties. A DNA sequence (see also AATG2524) in which the ACTH coding region of the POMC gene is delated its preferred. Host cells transformed with vectors (or a single polycistronic vector) encoding analgesic cpds. can be encapsulated to form bioartificial organs that are implanted into a patient for control of pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianamentc; antiarthritic; cancer; antisheumatic; hepatotropic, cereborprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparastitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human nervous system related polynucleotide SEQ ID NO 11509.
                                                                                                                                                                                                                                                                                                         Sequence 849 BP; 176 A; 266 C; 286 G; 121 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                             Length 849;
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                           0.9%; Score 20; DB 2; Le:
100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 GCAACAGCAGCAGCAGCGGC
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2000US-0225267P.
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                                                                                                                                                                                                                                                                                                                                                                                                                             20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 20; Conserv
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14-AUG-2000;
14-AUG-2000;
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ABA19178/c
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Mon Mar 28 06:06:56 2005

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2000US-025268P.
2000US-022547P.
2000US-022547P.
2000US-022578P.
2000US-022578P.
2000US-022578P.
2000US-022688P.
2000US-022688P.
2000US-022688P.
2000US-022688P.
2000US-022688P.
2000US-02298P.
2000US-02298P.
2000US-022944P.
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2000US-0233401P

2000US-023364P

2000US-023365P

2000US-0234233P

2000US-0234233P

2000US-023424P

2000US-023424P

2000US-023424P

2000US-023424P

2000US-023484P

2000US-023584P

2000US-023584P

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2000US-02358P

2000US-02358P

2000US-02358P

2000US-023703P

2000US-0231703P

2000US-0231703P

2000US-0231703P

2000US-0231703P

2000US-0231703P

2000US-0231703P

2000US-0231703P

2000US-0231703P

2000US-024178F

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2000US-024178F
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2000US-0246474P
2000US-0246475P
2000US-0246476P
2000US-0246476P
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2000US-0246526P
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
18-AUG-2000; 2
22-AUG-2000; 2
23-AUG-2000; 2
30-AUG-2000; 2
30-AUG
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25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
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08-NOV-2000; 2000US-0246527P.
08-NOV-2000; 2000US-0246523P.
08-NOV-2000; 2000US-0246653P.
08-NOV-2000; 2000US-0246610P.
08-NOV-2000; 2000US-0246610P.
17-NOV-2000; 2000US-0246613P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-024921P.
17-NOV-2000; 2000US-024921P.
17-NOV-2000; 2000US-024921P.
17-NOV-2000; 2000US-024921P.
17-NOV-2000; 2000US-024926P.
17-NOV-2000; 2000US-024926P.
17-NOV-2000; 2000US-024926P.
17-NOV-2000; 2000US-024926P.
17-NOV-2000; 2000US-024926P.
17-NOV-2000; 2000US-02493P.
17-NOV-2000; 2000US-02493P.
17-NOV-2000; 2000US-025198P.
18-DEC-2000; 2000US-025198P.
18-DEC-2000; 2000US-025198P.
18-DEC-2000; 2000US-025198P.
                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA, Barash SC, Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-541565/60.
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Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases.

Disclosure; SEQ ID NO 11509; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: a) cancer. e.g. breast and covarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune consorder, autoimmune hawolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as wycardial ischeemias; (d) wound healing (e) infectious diseases such as viral, bacterial, fungal and parasitic infectious diseases such as viral, bacterial, fungal and parasitic the printed specification, but was obtained in electronic format directly con WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 900 BP; 123 A; 288 C; 293 G; 196 T; 0 U; 0 Other;

Query Match

0.9%; Score 20; DB 5; Length 900;

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8X888888X8
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                                                                                                                                                                                                                                                                                                              Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification, cancer; cytostatic; nootropic; neuroprotective; antiinflammatory; immunosuppressive; immunostimulant; antianglogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; anglogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hillan KJ, Roy MA;
                    Gaps
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                    Indels
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     Pred. No. 1.6e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                    Human PRO23 nucleotide sequence SEQ ID NO:64.
                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 50; Fig 45; 286pp; English.
                                                                                    764 GCAACAGCAGCAGCGGC 745
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                       ;
                                                                                                                                                                                 AAC58389 standard; cDNA; 908 BP
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99WO-US012252.
99US-0141037P.
                                                        GCAACAGCAGCAGCGGC
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2000WO-US000219.
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         100.08;
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                                                                                                                                                                                                                                                       (first entry)
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Wood WI;
                         20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-572270/53.
P-PSDB; AAB24079.
         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-DEC-1999;
                                                                                                                                                                                                                                                       29-JAN-2001
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                                                                                                                                                                                                                      AAC58389;
                                                            43
                           Matches
                                                                                                                                                                 AAC58389
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astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunologic disorders. AGCSB242 to AACSB356 represent PCR primers and hybridisation probes used in the isolation of the human PRO sequences. AACSB367 to AACSB367 to AABCSB367 to AABCSB367 to AACSB36 and AAB24057 to AAB24089 represent human PRO polynucleotide and protein sequences given in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; pro-opiomelanocortin; POMC; corticosteroid; pain; analgesic;
chronic inflammation; neuroendocrine; CRF; beta-endorphin; gene therapy;
corticotrophin-releasing factor; antiinflammatory; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agent for reducing pain, useful particularly for chronic inflammatory pain, comprises a nucleic acid construct for local expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 936;
                                                                                                                                                                                                                                                                                                  Length 908;
                                                                                                                                                                                                                                   Sequence 908 BP; 173 A; 308 C; 310 G; 117 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wittig B, Stein C, Schaefer M, Schroff M, Junghans C;
Koenig Merediz SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human pro-opiomelanocortin coding sequence fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.9%; Score 20; DB 6; Ler
                                                                                                                                                                                                                                                                                            0.9%; Score 20; DB 3; Ler
100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 GCAACAGCAGCAGCAGCGGC 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 GCAACAGCAGCAGCAGCGGC 273
                                                                                                                                                                                                                                                                                                                                                                                                                  43 GCAACAGCAGCAGCGGC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 22; Page 33; 34pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
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Best Local Similarity 100.0
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-682796/73.
                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                       present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200267996-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuropeptides
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                                                                                                                                                                                                                                                                                                                                                                20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAL49917;
                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                Matches
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapp. The human colorance of the invention may have a use in gene therapp. The human against the against a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorder, endocrine cutoimmune/inflammatory disorder, developmental disorders, endocrine disorder, neurological disorders, developmental disorders, or clinections caused by virus, bacteria, fungi or parasite. The ditup from minter biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germine polymorphisms, as molecular weight markers, and for somatic or germine content the invention. Note: The sequence data for this patent is not represented the invention of specification, but was obtained in electronic format chiractly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                    Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Hartbikorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Patury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          New diagnostic and therapeutic polymucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human diagnostic and therapeutic polynucleotide SEQ ID NO:888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 1038; 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1038 BP; 208 A; 345 C; 355 G; 130 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O.9%; Score 20; DB Local Similarity 100.0%; Pred. No. 1.6 es 20; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page; 190pp; English.
                                                                                                      12-SEP-2003; 2003WO-US028227.
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                                                                                                                                            12-SEP-2002; 2002US-0410259P.
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P-PSDB; ABM83362.
                                                                                                                                                                                                (INCY-) INCYTE CORP.
                               WO2004023973-A2
Homo sapiens.
                                                                     25-MAR-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIL16176-ABIJ1051), expressed DNA sequences (ABIL16176-ABIJ1051), expressed DNA ABIJ2072). The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
dithp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ds.
                                                                                                                                                                       Drosophila melanogaster genomic polynucleotide SEQ ID NO 32866.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 984;
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0.9%; Score 20; DB 4; Le Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matchles 20; Conservative 0; Mismatchles 0;
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                                                            ABL27131 standard; DNA; 984 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li PWD,
                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US009231.
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11-JUL-2000; 2000US-00614150.
                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                               Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-656860/75.
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                                                                                                                                    26-MAR-2002
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                                                                                                ABL27131;
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ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
dithp.
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                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human diagnostic and therapeutic polynucleotide SEQ ID NO:887.
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.00.0%; Pred. No. 1.6e+02;
.ve 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                               Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-SEP-2003; 2003WO-US028227.
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12-SEP-2002; 2002US-0410260P.
                                                                                                                                                                                       23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                       23-MAR-2001; 2001WO-US009231
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Best Local Similarity 100."
Matches 20; Conservative
Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                               Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INCY-) INCYTE CORP.
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                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY.
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                                               WO200171042-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            interactions
                                                                                               27-SEP-2001
                                                                                                                                                                                                                                                                                                               Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACN42012;
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ACN42012
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                                                                                                                                                                                                                                                                                                               Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Blder LV;
Mononey EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RB, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Patury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.9%; Score 20; DB 13; Length 1039; 00.0%; Pred. No. 1.6e+02; ve 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page; 190pp; English.
                                                                                                                                                                                                   2002US-0410259P.
2002US-0410260P.
                                                                                                                                                      12-SEP-2003; 2003WO-US028227
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                                                                                                                                                                                                                                                                            (INCY-) INCYTE CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in gene mapping.
                                                         WO2004023973-A2
            Homo sapiens.
                                                                                                                                                                                                      12-SEP-2002;
12-SEP-2002;
                                                                                                         25-MAR-2004
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Best Local S
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RESULT 61

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Gaps

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Myers EW;

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therappy. The human diagnostic and therapeutic polynucleotides (dithp) or polypepides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorder, developmental disorders, or disorder, interological disorders, developmental disorders, or infections caused by virus, beatrointestinal disorders, or infections caused by virus, partering aftering in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp polynucleotide of the invention. Note: The sequence data for this patent is not represented the printed specification, but was obtained in electronic format the present was used to the present sequence data for this patent is not represented the printed specification, but was obtained in electronic format caused the present sequence are sequenced.
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP; Stevens RA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH; Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL, Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES; Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
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                                                                                                                                                                                                        New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
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dithp.
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SJ, Elder LV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human diagnostic and therapeutic polynucleotide SEQ ID NO:886.
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Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1088 BP; 219 A; 358 C; 368 G; 143 T; 0 U; 0 Other;
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les 0; Indels
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Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ,
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                                                                                                           Suarez CJ;
                                                                                                                                                                                                                                                                                                            Claim 1; Page; 190pp; English.
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12-SEP-2002; 2002US-0410260P.
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                                                                                                                                             WPI; 2004-329368/30.
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                                                                                   Xu Y, Kwong M, Po
Patury S, Shi X,
                                                                                                                                                                  P-PSDB; ABM83360
                                                                                                                                                                                                                                                                         gene mapping.
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therappy. The human polynucleotide of the invention may have a use in gene therappy. The human condition, disease or disorder associated used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorder, endocrine autoimmune/inflammatory disorder, developmental disorders, or disorder, autoimmune/inflammatory disorder, developmental disorders, or disorder, disorder, disorders, or infections caused by virus, bacteria, fungi or parasite. The dituper of infections caused by virus, bacteria, fungi or parasite. The dituper of molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide of polymorphisms, as molecular weight markers, and for somatic or germine gene therapy. The present sequence represents a ditup polynucleotide of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format currently from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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                                                                                                                                                                                                                                    New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP, Stevens KA, Blanchard JL, Panzer SK, Wang X, Au AP, Gerstin EH; Beralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Legece RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES; Xuu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen Jatury S, Shi X, Suarez CJ;
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100.0%; Pred. No. 1.6e+02;
iive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1089 BP; 229 A; 350 C; 360 G; 150 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page; 190pp; English.
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                                                                                                                                                                WPI; 2004-329368/30.
P-PSDB; ABM83359.
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ID AAZ2
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98US-0078563P.

19-MAR-1998;

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RESULT 66
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                                                                                                                                                                                                                                                                                                    This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAZ24802) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 95 novel genes and their fragments (mucleic acid sequences: AAZ24811-Z24907; amino acid sequences AAY41308-Y41404) which are useful for preventing, treating acid sequences AAY41308-Y41404) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polympeides in a sample or by determining the presence of mutations in the new polymucleotides. Specific uses are described for each of the 95 polymucleotides, based on which tissues they are most highly expressed in (see AAZ24811 for described uses)
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                                                                                                                                                         DR;
Olsen HS;
                                                                                                                                                                                                                                       New isolated human genes, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood
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                                                                                                                                                           Yu G, Young PE, Feng P, Soppet
, Kyaw H, Ebner R, Lafleur DW,
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                                                                                                                                                                                                                                                                                     Claim 1; Page 340-341; 484pp; English.
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                                             9805-0078577P
9805-0078578P.
9805-0078579P.
9805-0078581P.
9805-0080312P.
9805-0080312P.
                                                                                                                                                            Ni J, Rosen CA, Y
dress GA, Duan RD,
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             98US-0078573P.
98US-0078574P.
98US-0078576P.
                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                        WPI; 1999-562050/47.
                                                                                                                                                                         Endress GA,
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Best Local Similarity
                                                                                                                                                                         Wei Y, Endress GA
Shi Y, Moore PA;
                                                                                                                                                                                                                    P-PSDB; AAY41377.
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                                   19-MAR-1998;
19-MAR-1998;
19-MAR-1998;
19-MAR-1998;
19-MAR-1998;
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                                                                                           01-APR-1998;
01-APR-1998;
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                           19-MAR-1998
                                                                                                                                                                                                                                                                  disorders.
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Matches
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                                                                                                                                                                                                              Novel isolated and purified nucleic acid molecule encoding beta-
endorphin, useful for treating a patient for psychological dependence on,
and abuse of, substances which have a stimulating and euphoric effect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOVX; antidiabetic; anorectic; cardiant; hypotensive; antidiabetic; virucide; antibacterial; fungicide; protozoacide; nootropic; neuroprotective; antibarkinsonian; anticonvulsant; osteopathic; antiarthritic; antiinflammatory; dermatcological; antiarthritic; metabolic; diabetes; obesity; infectious; anorexia; cancer; cardiovascular; hypertension; atheroselerosis; neurodegenerative; Alzhaimer's disease; Parkinson's; epilepsy; immune; neurogenerative; Alzhaimer's disease; Parkinson's; epilepsy; immune; neurogenesis; cell differentiation; proliferation; haemopoiesis; wound healing; anglogenesis; gene therapy; chromosome mapping;
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0.9%; Score 20; DB 3; Length 1230;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1230 BP; 265 A; 379 C; 411 G; 175 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 3-4; 8pp; Norwegian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue typing; human; ss; gene; NOV
                                                                                                          Berg K;
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2001US-0341346P.
2001US-0341477P.
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2001US-0342592P.
2001US-0344297P.
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2002US-0373288P.
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98NO-00004992
                                                                                                          Fagerlund TH, Alestrom P,
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                                                                                                                                                                    WPI; 2000-373908/32
                                                      (GENO-) GENOVA AS.
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17-APR-2002;
15-MAY-2002;
27-OCT-1998;
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20-DEC-2001;
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12-DEC-2001;
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Human, NOVX; gene; ss; congenital heart defect; cardiomyopathy; atherosels; Appertension; pulmonary stenosis; scleroderma; adenocarcinoma; haemophilia; graft-versus-host disease; cancer; neurodegenerative disorder; Alzheimer's disease; parkinson's disease; multiple sclerosis; diabetes; obeatty; bronchial asthma; acquired immunodeficiency syndrome; AlDS; Crohn's disease; infectious disease; anorexia; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-2001, 2001US-00035568.
05-NOV-2001; 2001US-033662P.
09-NOV-2001; 2001US-033662P.
09-NOV-2001; 2001US-033610P.
21-NOV-2001; 2001US-033610P.
21-NOV-2001; 2001US-0335152P.
28-NOV-2001; 2001US-0331312P.
29-NOV-2001; 2001US-0331312P.
29-NOV-2001; 2001US-0331312P.
29-NOV-2001; 2001US-033130P.
15-MAY-2002; 2002US-039148P.
02-JUL-2002; 2002US-039148P.
02-JUL-2002; 2002US-039148P.
03-JUL-2002; 2002US-039162P.
06-AUG-2002; 2002US-0401479P.
06-AUG-2002; 2002US-040152EP.
07-AUG-2002; 2002US-040152EP.
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ALVAREZ E.
ANDERSON D W.
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LEPLEY D M.
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BURGESS C E.
CASMAN S J.
CHAPOVAL A.
DHANABAL M.
EDINGER S R.
EISEN A.
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ETTENBERG S.
GANGOLLI E A.
GERLACH V.
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MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MCQUEENEY K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PADIGARU M.
PATTURAJAN N
PENA C E A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GORMAN L.
GROSSE W M.
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MILLER C E.
MILLET I.
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                                                                                                                                                                                                                                                                       JS2004067882-A1.
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                                                                                                                                                                                                                     Homo sapiens.
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(ALVA/)
(ALVA/)
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(BURG/)
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(CHAP/
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(MCQU/)
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KHRA/)
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           The invention relates to a novel isolated NOVX polypeptide. The polypeptide of the invention demonstrates, antidiabetic, anorectic, cardiant, hypotensive, antiarteriosclerotic, virucide, antiparterial, fungicide, proteozoacide, noctropic, neuroprotective, antiparkinsonian, anticonvulsant, osceopathic, antiarthritic; antipartamatory functional anticonvulsant, osceopathic, antilatomatic and antilipaemic activities. The polypeptides, nucleic acid molecules and antilipaemic activities. The polypeptides, nucleic acid molecules and antilogement of secrets and observed infections diseases including metabolic disorders such as cradiovascular diseases including metabolic disorders such as cardiovascular diseases including mypertension and atherosclerosis, cardiovascular diseases including hypertension and atherosclerosis, cardiovascular diseases including hypertension and atherosclerosis, neurodegenerative disorders such as Alzabiamer's disease, Parkinson's disease and epilepsy, immune disorders, asthma and dyslipidaemia.

The neurodegenerative disorders and polypeptides may also be used to identify molecules that modulate or inhibit neurogenesis, cell anglogenesis, as well as in gene therapy. Finally, the nucleic acids may be used as hybridiation probes, in chromosome mapping, tissue typing, the human NOV cDNA of the invention.
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                                                                                                                                                                                                                                                                             Alsobrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL; Burgess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A; Elerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L; Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV; Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, Mcqueeney K; Mezes SS, Miller CE, Millet I, Mishra VS, Padigaru M, Patturajan M; Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA; Smithson G, Starling G, Spytek KA, Stone DJ, Tchernev VT, Twomlow N; Vernet CAM, Zerhusen BD, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated NOVX polypeptides and polynucleotides, useful for .. reventing, diagnosting or treating NOVX-associated disorders, e.g. osteoarthitis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.9%; Score 20; DB 10; Length 12
100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 37; 447pp; English.
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17-MAY-2002; 2002US-0381495P.
28-MAY-2002; 2002US-0383534P.
29-MAY-2002; 2002US-0383629P.
29-MAY-2002; 2002US-0384024P.
07-MUS-2002; 2002US-0401788P.
26-AUG-2002; 2002US-0401788P.
31-OCT-2002; 2002US-0401537P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-2004 (first entry)
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                                                                                                                                                                                                                                    (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2003-441555/41.
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Matches
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XEXEXEX

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Burgess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A; Ellerman K, Ettenberg S, Gangolli EA, Gerlach V, Gorman L; Grosse WM, Guo X, Hackett C, Di W, Kekuda R, Khramtsov NV; Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, Mcqueeney K; Meze PS, Miller CE, Miller I, Mishra V, Padigaru M, Patturajan M; Pena CEA, Peyman JA, Rastelli L, Rieger DK, Rothenberg ME; Shenoy SG, Shimkers RA, Sutthson G, Spaderna SK, Stanling G; Spytek KA, Stone DJ, Tchernev VT, Twomlow N, Vernet CAM; Cerhusen BD, Voss EZ, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                  Novel isolated NOVX polypeptide useful treating or preventing disorders or syndromes such as Alzheimer's disease, Parkinson's disease, multiple sclerosis, diabetes, obesity, cancer, bronchial asthma, Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1245 BP; 170 A; 486 C; 407 G; 182 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 37; 330pp; English.
PEYMAN J A.
RASTELLI I.
RIEGER D K.
ROTHENBERG M E.
SHENOY S G.
SHIMKETS R A.
SHIMKETS R A.
SMITKEON G.
SPADERNA S K.
STARLING G.
SPATER K A.
STONE D J.
                                                                                                                                                  VERNET C A M.
ZERHUSEN B D.
VOSS E Z.
                                                                                                                                                                                                                                                                                                                                   WPI; 2004-355303/33.
                                                                                                                                      TWOMLOW N.
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                                                                                                                                                                                   ZHONG M.
                                              (SHEN/)
(SHIM/)
(SMIT/)
                                                                                           (STAR/)
(SPYT/)
(STON/)
(TCHE/)
(TWOM/)
                                                                                                                                                                        (VOSS/)
                                                                                                                                                   (VERN/)
(ZERH/)
                                                                               (SPAD/)
                        RIEG/)
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The invention relates to human NOVX polypeptides and the polynucleotides are useful for encoding them. The NOVX polypeptides and polynucleotides are useful for determining the presence of or predisposition to a disease associated with altered levels of the sequences in a mammalian subject, and for treating or preventing a pathology associated with NOVX. The polypeptides are useful for treating or preventing disorders or syndromes such as congenital heart defects, cardiomyopathy, atheroscierosis, hypertension, pulmonary stenosis, soleroderma, adenocarcinoma, haemophilia, graft-versus-host disease, cancer, neurodegenerative disorders, Alzheimer's disease, parkinson's disease, multiple sclerosis, diabetes, obesity, bronchial asthma, acquired immunodeficiency syndrome (AIDS), Crohn's disease, human NOVX polynucleotide of the invention. Note: The sequence data for this patent is also available from USPTO at sequence represents a human NOVX is also available from USPTO at sequence.
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Pred. No. 1.5e+02;
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100.0%; Pred
0; M
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nes 20; Conservative
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ARCT99126 to ACC79105 encode the human secreted proteins (I) given in ARE56726 to ABR56805, designated SECP-1 to SECP-80. SECP sequences can have cytostatic, antiateriosclerotic, anticonvulsant, antihillammatory, notropic, neuroprotective, crebroprotective, anti-HIV, antiallergic and thyromimetic activities, and can be used in gene therapy. The SECP proteins and polymucleotides can be used in diagnosing, treating and expression or conditions associated with the decreased expression or overexpression of SECP, such as cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS, allergies) and developmental (e.g. hypothyroidism, Cushing's syndrome) disorders, or infections. They are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of SECP. The SECP or its fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polynucleotide and compounds that specifically bind to or modulate the activity of the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1418 BP; 168 A; 542 C; 442 G; 266 T; 0 U; 0 Other;
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138 GCAACAGCAGCAGCAGCGGC 119

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62

GCAACAGCAGCAGCGGC

43

BP.

ACC79031/c ID ACC79031 standard; cDNA; 1418 XX AC ACC79031; AC ACC79031; DT 30-JUL-2003 (first entry)

Length 1418; 0.9%; Score 20; DB 10; 100.0%; Pred. No. 1.5e+02; Best Local Similarity Query Match

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anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiallergic; antiinflammatory; thyromimetic; gene therapy; cancer; cell proliferative disorder; atherosclerosis; neurological disorder;
                                                                                          epilepsy; Huntington's disease; stroke; immune disorder; allergy; AIDS; inflammatory disorder; developmental disorder; hypothyroidism; Cushing's syndrome; infection; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human secreted proteins (SECP), useful for diagnosing, treating preventing diseases or conditions associated with the aberrant SECP expression e.g. cancer, AIDS, atherosclerosis, Huntington's disease, stroke, infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lal PG, Yue H, Honchell CD;
Baughn MR, Duggan BM, Tran UK;
TW, Lee S, Thangavelu K, Yue H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lehr-Mason PM, Bufford N, Xu Y, Baughn MR, Duggan BM, Iran un; Lehr-Mason PM, Bufford N, Richardson TW, Lee S, Thangavelu K, Yue H Emerling BM, Walla NK, Azimzai Y, Sanjanwala B, Hafalia AJA; Borowsky ML, Nguyen DB, Ison CH, Astromoff A, Ding L, Lee SY; Becha SD, Ramkumar J, Gandhi AR, Jin P, Fu GK, Swarnakar A;
                                    secreted protein; SECP; cytostatic; antiarteriosclerotic;
          Human secreted protein SECP-6 encoding cDNA SEQ ID NO:86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gietzen KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 246; 286pp; English.
                                                                                                                                                                                                                                                             17-AUG-2001; 2001US-0313249P.
24-AUG-2001; 2001US-0314752P.
07-SEP-2001; 2001US-031781BP.
21-SEP-2001; 2001US-0317824P.
21-SEP-2001; 2001US-0324586P.
02-NOV-2001; 2001US-034586P.
28-NOV-2001; 2001US-0343980P.
28-NOV-2001; 2001US-03439P.
13-FEB-2002; 2002US-0356041P.
19-MAR-2002; 2002US-0366041P.
                                                                                                                                                                                                                                                                                                                                                                                                                      2002US-0376988P
                                                                                                                                                                                                                                    15-AUG-2002; 2002WO-US027143
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Warren BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-278569/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; ABR56731
                                                                                                                                                                                 WO2003016506-A2
                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                           27-FEB-2003
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Plant; maize; rice; sorghum; thale cress; soybean; wheat; transgenic; osmocic stress; sugar transport; call cycle pathway; plant height; carbohydrate transport; crop productivity; plant growth; stress resistance; disease resistance; insect resistance; insect nitrogen assimilation; water stress tolerance; photocosynthetic carbon fixation; virus resistance; gene therapy; gene; ds.
                     Polynucleotide sequence #280 useful in producing transgenic plants.
                                                                                                                                                                                                                                                        04-DEC-2002; 2002US-00310154.
                                                                                                                                                                                           UŠ2003233670-A1.
                                                                                                                                                               Oryza sativa.
                                                                                                                                                                                                                            18-DEC-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA71941
ID ADA7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention i useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequence data for this parter did not form part of the printed specification, but was obtained in electronic form part of the from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                      Drosophila melanogaster expressed polynucleotide SEQ ID NO 7061.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20; DB 4; Length 1565;
Pred. No. 1.5e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 7061; 21pp + Sequence Listing; English.
   Indels
   ö
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.0%; Pred. No. 1.5 hes 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myers EW;
                                                            138 GCAACAGCAGCAGCAGCGGC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 GCAACAGCAGCAGCGGC 253
                                62
                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
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0
                              43 GCAACAGCAGCAGCAGCGGC
                                                                                                                                         ABL04193 standard; cDNA; 1565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 GCAACAGCAGCAGCAGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADM47862 standard; DNA; 1891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 98:0
                                                                                                                                                                                                      (first entry)
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20; Conservative
                                                                                                                                                                                                                                                                                       pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-656860/75.
P-PSDB; ABB60090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                  WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interactions.
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                                                                                                                                                                                                        26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2001.
                                                                                                                                                                         ABL04193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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 Matches
                                                                                                           RESULT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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The present invention relates to polynucleotide sequences, and the proteins they encode. The sequences are isolated from a variety of proteins they encode. The sequences are isolated from a variety of organisms such as plants (e.g. maize, rice, sorghum, thale cress, cognes, and wheat), cyanobacteria, bacteria, yeast and other fungi. The polynucleotide and polypeptide sequences of the invention are useful in the production of transgenic plants that have improved properties. Also disclosed are methods of producing fertile transgenic plants, preferably maize, with desired phenotypes. The polynucleotide and polypeptide sequences are useful for improving plants by providing protection against compitying the cell cycle pathway, reducing plant height, modifying the cell cycle pathway, reducing plant height, modifying crop productivity, improving plant carbohydrate transport, improving disease resistance, improving disease resistance, improving crop productivity, improving plant sets resistance, improving crop heat tolerance, improving stalk strength, improving water stress tolerance, improving resistance to oxidative stress tolerance, improving resistance to oxidative stress tolerance, improving resistance to oxidative stress providing increased vigour, reducing sensecence, and conferring virus resistance. The present sequence represents a polynucleotide sequence of the invention. Note: The sequence data for this patent is not provided in the printed apecification but is obtained in electronic format from the USPPO website at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide, useful for manipulating plant protein quality, improving plant growth, yield and crop productivity or grain composition or producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1891 BP; 379 A; 669 C; 494 G; 349 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 280; 144pp; English.
                                                                                                                                                                                                                                                                           Laccetti LB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1125 GCGCAACAGCAGCAGC 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 GCGGCAACAGCAGCAGC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA71941 standard; DNA; 2000 BP.
04-DEC-2001; 2001US-0337358P.
                                                                                                                                                                                                                                                                     Edgerton MD, Chomet PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20; Conservative
                                                                             (EDGE/) EDGERTON M D. (CHOM/) CHOMET P S. (LACC/) LACCETTI L B.
                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-061374/06.
P-PSDB; ADM48230.
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The invention relates to plant nucleotide sequences that direct seed.,

c leaf- and/or stem., panicle., root- or pollen-specific or -preferential

c c constitutive transcription of an operatively linked nucleic acid

c segment. The invention also relates to a method for augmenting a plant

c segment. The seed, leaf, stem, panicle, pollen, root or is constitutive

c altered in the seed, leaf, stem, panicle, pollen, root or is constitutive

c altered in the seed, leaf, stem, panicle, pollen, root or is constitutive

c altered in the seed, leaf, stem, panicle, pollen, root or is constitutive

c altered in the seed, leaf, stem, panicle, pollen, root or is constitutive

c an a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,

c cancla, cotton, peanut, tobacco or sugar beet, preferably maize, barley,

c corghum, rice or wheat. The polynucleotides and the polypeptides they

c encode are useful for manipulating crop plants to alter or improve

c phenotypic characteristics, to produce large quantities of oil or

c proteins, to incur resistance to insecticides, viruses or fungi, and to

c incur stress tolerance (e.g. salt, cold or drought) to ensure the plants

c incur stress tolerance (e.g. salt, cold or drought) to ensure the plants

c incur stress tolerance (e.g. salt, reduced apical dominance or dwarfism,

c arly flowering or altered metabolic pathways. This sequence appresents a

constitution part of the pinnention. Note: The sequence apprentic a

c plant nucleic acid of the invention. Note: The sequence apprent of or electronic format directly from USPTO at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance or high nutritional value.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moughamer T, Briggs SP, Cooper B, Glaz
tagiri F, Kreps J, Provart N, Ricke D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 44; SEQ ID NO 2021; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 TGCTGATGGTGATGGAGATT 303
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                                                                                                                                               26-SEP-2001; 2001US-0325277P.
26-SEP-2001; 2001US-0325448P.
04-APR-2002; 2002US-0370620P.
                                                                                                     26~SEP-2002; 2002US-00260238.
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                                                                                                                                                                                                                                                                                                                             GLAZEBROOK J.
GOFF S A.
KATAGIRI F.
                                                                                                                                                                                                                                                          MOUGHAMER T.
BRIGGS S P.
COOPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-190374/18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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PROVART N.
RICKE D.
ZHU T.
                    US2004016025-A1
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                                                            22-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goff SA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                            (RICK/)
(ZHUT/)
                                                                                                                                                                                                                                            BUDW/)
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                                                                                                                                                                                                                                                                                                                                                                                                KREP/)
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                                                                                                                                                                                                                                                                                                                                  GLAZ/)
                                                                                                                                                                                                                                                                                                                                                    (GOFF/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, funginous viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant, gene; ss; transcription; plant genome augmentation; cereal; soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet; amize; barley; sorghum; rice; wheat; crop plant; insecticide resistance; stress tolerance; cold tolerance; drought tolerance; plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   t t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                 Plant; bacterial infection; fungal infection; viral infection; rice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zon G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.9%; Score 20; DB 8; Length 2000;
100.0%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glazebrook J, Goff SA, Hov
Whitham S, Xie Z, Zhu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID NO 5266; 899pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 TGCTGATGGTGATGGAGATT 303
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S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                                                  22-JUN-2001; 2001WO-IB001105
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                                                20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention
                                                                                        Rice gene, SEQ ID 5266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chang H, Chen W, Co
Katagiri F, Quan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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illustrate the
                                                                                                                                                                                                       Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-2004
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antifungal
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    ADA71941
                                                                                                                                                               gene; da.
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Matches

ð g ADJ41021

Glazebrook J;

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                                 0.9%; Score 20; DB 12; Length 2000; 100.0%; Pred. No. 1.5e+02; vative 0; Mismatches 0; Indels C
Sequence 2000 BP; 649 A; 375 C; 340 G; 630 T; 0 U; 6 Other;
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EP1074617-A2. Homo sapiens.

07-FEB-2001.

29-JUL-1999;

Ota T, Is Ishii S,

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The invention relates to isolated polymucleotide (I) and polypeptide (II)

sequences. (I) is useful as hybridiaation probes, polymerase chain

creation (PCR) primers, oligomers, and for chromosome and gene mapping,

and in recombinant production of (II). The polymucleotides are also used

in diagnostics as expressed sequence tags for identifying expressed

confirmed to sexpressed sequence tags for identifying expressed

confirmed to sexpressed sequence tags for identifying expressed

confirmed to severating antibodies against it, detecting or quantitating a

confirmed to sequences are useful in medical imaging

confirmed to propopting the intensity and its binding partners are useful for treating disorders

confirmed and polymucleotide sequences have applications in

polypeptide and polymucleotide sequences have applications in

confirmed and polymucleotide sequences have applications in

confirmed to produce other types of data and products dependent on DNA and

confirmed and polymucleotide sequences or other traits to assess biodiversity

and to produce other types of data and products dependent on DNA and

confirmed and polymucleotide sequence data for this

confirmed and polymucleotide sequences or other traits to assess biodiversity

and to produce other types of data and products dependent on DNA and

confirmed and polymucleotide sequence data for this

confirmed and polymucleotide sequences or the invention. Note: The sequence data for this

confirmed and polymucleotide sequences or the invention and specification, but was obtained in

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confirmed and polymucleotide dependences and the printed dependences and the printed dependences and the printed dependences and the printed dependences
                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.9%; Score 20; DB 5; Length 2370;
100.0%; Pred. No. 1.5e+02;
iive 0; Mismatches 0; Indels
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                                      DNA encoding novel human diagnostic protein #7939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 7939; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ormanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; ABG07948.
                                                                                                                                                                                                                                                       WO200175067-A2.
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                                                                                                                                                                                                  Homo sapiens
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EXEXEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polymucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the compination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polymucleotide which comprises a 5'-end complementary strand of a polymucleotide which comprises a 5'-end polymucleotide comprises a 3'-end sequence complementary to a polymucleotide comprises a 3'-end sequence complementary to a polymucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers are as an eased in antisense therapy and in gene therapy. The primers are and an ensure set and an ensure the complementary to particularly full-length cDNAs. The primers are also useful for the primers and or disgnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH3363 to AAH13633 to AAH18633 to AAH18631 to AAH18632 represent human amino acid sequences; and AAH13629 to AAH33629 and consecution in the exemplification of the process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                        Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; SEQ ID NO 18501; 2537pp + Sequence Listing; English.
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0.9%; Score 20; DB 4; Length 2370;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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Human cDNA sequence SEQ ID NO:18501
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11.JAN-2000; 2000JP-00118776.
02.MAY-2000; 2000JP-00133767.
09-JUN-2000; 2000JP-00241899.
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ID AAS72135 standard; cDNA; 2370
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AAS72135;

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The invention comprises the amino acid and coding sequences of proteins which have enzyme activity or protease, phosphodiesterase, transferase, or isomerase inhibitor activity. The DNA and protein sequences of the invention are useful for treating disorders associated with the proteins, such as blood clotting or circulatory disorders. The present DNA sequence represents a novel mouse gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protease inhibitors, proteases, phosphodiesterases, transferases, isomerases and substances that affect their activity or expression useful for treating associated disorders.
   novel protein; enzyme; blood clotting disorder; circulatory disorder; mouse; murine; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2803 BP; 546 A; 848 C; 854 G; 555 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; SEQ ID NO 15; 524pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y, Kamiya M, Kubodera H;
                                                                                                                                                                                           26-ARR-2002; 2002JP-00126250.
30-ARR-2002; 2002JP-0012657.
02-MAY-2002; 2002JP-00130702.
02-MAY-2002; 2002JP-00130918.
02-MAY-2002; 2002JP-00130918.
04-DEC-2002; 2002JP-0035236.
04-DEC-2002; 2002JP-00352559.
04-DEC-2002; 2002JP-00352559.
04-DEC-2002; 2002JP-00352569.
04-DEC-2002; 2002JP-00352694.
04-DEC-2002; 2002JP-00352694.
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(DNAF-) DNAFORM KK.
(MITU ) MITSUBISHI CHEM CORP.
                                                                                                                                                18-APR-2003; 2003WO-JP004983
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                                                                                        WO2003089644-A1.
                                                          Mus musculus.
                                                                                                                                                                                 19-APR-2002;
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Query Match

0.9%; Score 20; DB 12; Length 2803;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps

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43 GCAACAGCAGCAGCAGCGGC 62

338 GCAACAGCAGCAGCAGCGGC 319

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Sequence 1791, Appli
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       GenCore version 5.1.6
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US-09-903-216-3
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US-09-903-199-3
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US-10-086-534-37
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301 ATTTTGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAAGAGAGATCTACTTCAGAGC 360

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Qy 1441 ATGAAGAGCTGACACCTAATGATGGCTTTGCTAAAGTCCATTAAGGCTTCA 1500 1441 ATGAAGAGGTGCTGAGTGTGACACCTAATGATGGCTTTGCTAAAGTCCATTATGGCTTCA 1500	Oy 1501 TCCTGAAGGAACAAATTGCTGAGAGCATCCCATATTTAAAGGAAGG	Qy 1561 CCGGAGATCCTGGCACTGATGATGATTTTATTTCCACCTGGGGGATGCCATGCAGA 1620 Db 1561 CCGGAGATCCTGATGATGAGAGATTTTATTTCCACCTGGGGAATGCCATGCAGA 1620	OY 1621 GGGTTGGGAACAAAGAGGCATATAAGTGGTATGAGCTTGGGCACAAGAGACACACTTTG 1680	Qy 1681 CATCTGTCTGGCAACGCTCACTCTACAATGTGAATGGACTGAAAGCACCTTGGTGGA 1740	Qy 1741 CCCCAAAAGAAACGGGCTACACAGAGTTAGTAAAGTTTTAGAAAGAA	Qy 1801 TCCGAGATGAAGGCCTTGCAGTGATGAAAGCCAAAGGTCTCTTCCTGCCTG	1861	OY 1921 ATGAAAATGCCTGCAAAGGAGCTCCTAAAAACCTGTACTAGAAAAGTTCCCCGAGA 1980	OY 1981 CAACAGGATGCAGAACAGATCAAATATTCCATCATGCACCCGGGACTCACGTGT 2040	2041	OY 2101 AGGAAGGCTGCAAGATTCGATGTGCCAACGAGACCAGGACCTGGGAAGGAA	Qy 2161 TCATCTTTGATGACTCCTTTGAGCACGAGGATGCCAGGATGCCTCATCTTCCGGCTGA 2220	Qy 2221 TATTCATCGTGGATGTGTGGCATCGGAACTGACACCACAGAGACGCAGCCTTCCAG 2280	Oy 2281 CANTTAGCATGAATTCATGCAAGCTTGGGAAACTCTGGAGAGA 2324	RESULT 4 US-09-903-216-3 Sequence 3, Application US/09903216	. ; FAUERL INCORMATION: ; APPLICANT: Wands, Jack R. ; APPLICANT: Wands, Sack R. ; APPLICANT: de la Monte, Suzanne M.	; APPLICANT: Ince, wedim ; APPLICANT: Carlson, Rolf I. ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS ; FILE REFERENCE: 21486-032 DIV2	
DD 301 ATTTGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAAGGAGGATCTACTTCAGAGC 360 Qy 361 CAGCAGTCCCGCCAGAAGAGGCTGAGCCACACACTGAGCCCGAGGAGGAGGTTCCTGTGG 420 DD 361 CAGCAGTCCCGCCAGAAGAGGCTGAGCCAACACACACACA	421 AGGCAGAACCCCAGAATATCGAAGATGAAACAAAAAAAATCAGTCCCTTCCCATG	AAATGGTACACGCAGAACATGTTGAGGAGAAGACACTTGCAACAAGAAGATGGACCCACAG 	541 GAGAACCACAACAAGAGGATGATGATTTTTTATGGCGACTGATGTAGATGTG 	601 AGACCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGA		721 ATTCCAGTGAACCAGTAGAAGATGAAAGATTGCACCATGATACAGATGTAACAT 	Qy 781 ACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAAATGAAGGGATAGAAATCA 840 Db 781 ACCAAGTCTATGAGGAACAAGGAGTATATGAACTCTAGAAATGAAGGGATAGAAATCA 840	QY 841 CAGAAGTAACTGCTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG 900 DD 841 CAGAAGTAACTGCTCCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG 900	901 AAGTAAGCATTTTTCCTGGAAGAACAGCAGGAAGTACCACCAGAAACAATAGAAAAA 	961	OY 1021 TTGATAAGACTATTAAAGCTGAACTTGATGCTGCAGAAAAACTCCGTAAAAGGGGAAAAA 1080 Db 1021 TTGATAAGACTATTAAAGCTGAACTTGATGCTGCAGAAAAACTCCGTAAAAGGGGAAAAA 1080	GTCCACGAG GTCCACGAG	CAAGATATGGGAAGGCGCAGTGTGAGGATGATTTGGCTGAGAAGAGGAGAAGTAATGAGG 	1201 IGCTACGIGGAGCCATCGAGACCTACCAGGGGGGCCAGCCTACCTGATGTCCCTGCGG 1260 	OY 1261 ACCTGCTGAAGCTGAGTTTGAAGCGTCGCTCAGACAACAATTTCTAGGTCATATGA 1320	OY 1321 GAGGTTCCCTGCTTACCCTGCAGAGATTAGTTCAACTATTTCCCAATAGATACTTCCTTAA 1380	OY 1381 AAAATGACCTTGGCGTGGGATACCTCTTGATAGGAGATAATGACAATGCAAAGAAAG	

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ive 0; Mismatches
   CURRENT APPLICATION NUMBER: US/09/903,216
CURRENT FILING DATE: 2001-07-11
PRIOR PILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENT VET. 2.1
SEQ ID NO 3
LENGTH: 2324
                                                                                                                      Query Match
Best Local Similarity 100.
Matches 2324; Conservative
                                                                                TYPE: DNA ORGANISM: Homo sapiens
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US-09-903-216-3
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APPLICANT: Carlson, Rolf I.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
FILE REPERRENCE: 21486-032 DIVI
CURRENT APPLICATION NUMBER: US/09/903,023
CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 09/436,184
PRIOR PILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 3
                                                                                                                                                                                                  100.0%; Score 2324;
llarity 100.0%; Pred. No. 0;
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Sequence 3, Application US/09903023;
Patent No. US20020146421A1
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne M
APPLICANT: Ince, Nedim

240 360 480 540 540 900 900 099 120 180 180 240 300 300 360 420 420 480 9 720 720 780 780 ACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAAAATGAAGGGATAGAAATCA 840 9 9 1 CGGACCGTGCAATGCCCAACGTAAGAATGCCAAGAGCAGCGGCAACAGCAGCAGCAGCG GCTCCGGCAGCGGTAGCACGAGTGCGGGCAGCAGCAGCCCCGGGGGCCCGGAGAGACAA THGTTGACTATGAGGAAGTTCTAGGAAACTAGGAATCTATGATGCTGATGGTGGAG TTGTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAGA 361 CAGCAGTCCCGCCAGAAGAGGCTGAGCCACACACTGAGCCCCGAGGAGCAGGTTCCTGTGG 421 AGGCAGAACCCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG AAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCACAG GAGAACCACAACAAGAGGATGATGATGAGTTTCTTATGGCGACTGATGTAGATGATAGATTTG CAGTITCACAAGACTGTAATCAGGATATGGAAGATGATGTCTGAGCAGGAAAATCCAG CAGITITCACAAGACIGIAATCAGGATATGGAAGATGATGTCTGAGCAGGAAAATCCAG ATTCCAGTGAACCAGTAGAAGATGAAAGATTGCACCATGATACAGATGATGTAACAT AGCATGGAGGACACAAGAATGGGAGGAAAAGGCGGACTCTCGGGAACTTCATTCTTCACGT GGTTTATGGTGATTGCTTGGCGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC GGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC ATTITGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAAAGAGAGATCTACTTCAGAGC ATTTTGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAAAGAGAGATCTACTTCAGAGC AGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG GAGAACCACAACAAGAGGATGATGAGTTTCTTATGGCGACTGATGTAGATTTG AGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGA 1 CGGACCGTGCAATGGCCCAGCGTAAGAATGCCAAGAGCAGCGGCAACAGCAGCAGCAGCG CAGCAGTCCCGCCAGAAGAGGCTGAGCCACACTGAGCCCCGAGGAGCAGGTTCCTGTGG ATTCCAGTGAACCAGTAGAAGATGAAAGATTGCACCATGATACAGATGATGTAACAT MALIGNANT NEOPLASMS ö 2324; Length Indels 661 721 721 781 엄 g ò ò

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g ;	4	AGAACCCCAGAATATCGAAGATGAAGACAAAAGAACAAATTCAGTCCCTTCTCCATG
B 5	481	AAATGGTACACCCAGAAACATGTTGAGGGAGAAGAACTTGCAACAAGAAGATGGACCCACAGG 340 AAATGGTACACGCGAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGAAGGTGGACCCACAG 540
8 8	ילח נ	GAGAACCACAACAAGAGATGATGATTCTTATGGCGACTGATGTAGATGTAGATTTG 600
3 8	ñ w	ANCONCANANTANGAGGAIGANGIII CII INIGAGGANCIGAT GINGALGANAGAII I GANGALIGANAGANA I I GANGALGANAGANA I I GANGALGANAGANA I I GANGALGANAGANA I GANGALGANAGANA I GANGALGANA ANGANAGANA ANGANAGANA ANGANAGANA ANGANAGANA
<u> </u>		AGACCITGGAACTIGAAGTATCTCATGAAGAAACCGAGGTAGGTACCACGTGGAAGAG 660
ò	. 661	ACTGTAATCAGGATATGGAAGAGATGATGTCTGAGCAGGAAAATCCAG
qq	661	TTCACAAGACTGTAATCAGGATATGGAAGAGATGATGTCTGAGCAGGAAAATCCAG
δ	72	CAGTAGTAGAAGATGAAAGATTGCACCATGATACAGATGATGTAACAT
q	721	TTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCATGATACAGATGATGTAACAT
ò	78	
අු	781	AGCAGTATATGAACCTCTAGAAAATGAAGGGATAGAAATCA
ò	841	NACTGCTCCCCTGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG
셤	841	IGAGGATAATCCTGTAGAAGATTCACAGGTAATTGTAGAAG
ð	06	AAGTAAGGATTTTTCCTGTGGAAGAACAGCAGGAAGTACCACCAGAAAAAAAA
qq	901	ragaaaa 9
à	96	AAATAAAT 1
qq	196	AAATAAAT 1
ò	102	TIGATAAGACTATTAAAGCIGAACTIGAIGCIGCAGAAAACTCCGTAAAAGGGGAAAAA 1080
Ω	1021	TGATAAGACTATTAAAGCTGAACTTGATGCTGCAGAAAAACTCCGTAAAAGGGGAAAAA 1
ò	108	TTGAGGAAGCAGTGAATGCATTTAAAGAACTAGTAGGAAATACCCTCAGAGTCCAGGG 1140
qq	ਜ	anddaadcagtgaatgcatttaaagaactagtacgcaaataccctcagagtccacgag
ò	1141	CAAGATATGGGAAGGCGCAGTGTGGGATGATTTGGCTGAGAAGAGGAGGAAGTAATGAGG 1200
qq	τ.	SATATGGGAAGGCGCAGTGTTGAGATGATTTGGCTGAGAAGAGGAGAAGTAATGAGG
ð	1201	GCTACGTGGAGCCATCGAGACCTACCAAGAGGTGGCCAGCCTACCTGATGTCCCTGCAG
q	ਜ	
δ	1261	CTGCTGAAGCTGAGTTTGAAGCGTCGCTCAGACAGGCAACAACAATTTCTAGGTCATATGA 1
q	1261	ACCTGCTGAAGCTGAGTTTGAAGCGTCGCTCAGACAAGGCAACAATTTCTAGGTCATATGA 1320
ò	. 1321	GAGGITCCCTGCTTACCCTGCAGAGATTAGTTCAACTATTTCCCCAATGATAA 1380
ф	1321	AGGTTCCCTG

AGTTT 1440 AGTTT 1440		- п	GCAGA 1620 GCAGA 1620	168 168	GTGGA 1740 GTGGA 1740	GTTAA 1800 GTTAA 1800	GGATG 1860 GGATG 1860	01 01	m m	CGTGT 2040 CGTGT 2040	TCCCA 2100	0 0	GCTGA 2220 GCTGA 2220	rrccag 2280 rccag 2280	
atgacaatgcaaaga atgacaatgcaaaga	CTAAAGTCCATTATG 	atttaaaggaaggaa' 	ACCTGGGGGATGCCA 	GGCACAAGAGGAGGAC 	TGAAAGCACAGCCTT TGAAAGCACAGCCTT	tagaaagaaactgga tagaagaaactgga	GTCTCTTCCTGCCTG 	TGTGGCAGCAAGGAA TGTGGCAGCAAGGAA	TACTAGAAAAGTTCC TACTAGAAAAGTTCC	TGCACCCGGGGACTC TGCACCCGGGACTC	ACCTGGGCTTGGTGA 	.cctgggaggaaggca .cctgggaggaaggca	ATGCCTCATCTTTCC 	'AGCAGAGGCAGCC 	AGAGA 2324 AGAGA 2324
CTCTTGATAGGAGATA 	CCTAATGATGGCTTTG 	SCTGAGAGCATCCCAT 	36GAGATTTTATTTCC 36GAGATTTTATTTCC	aagtggtatgaggttg aagtggtatgaggttg	TACAATGTGAATGGAC TACAATGTGAATGGAC	3agttagtaaagtett 	atggataaagccaaag 	rggagccagtrcacgc rggagccagtrcacgc	CCTAAAACCTGTACCT 	atcaaatattccatca atcaaatattccatca	IGCAGGCTCCGAATGC IGCAGGCTCCGAATGC	GCCAACGAGACCAGGA 	CACGAGGTATGGCAGG 	CCGGAACTGACACCAC 	GCTTGGGAAACTCTGC
aaaatgaccttggcgtgggatacctcttgataggagataatgacaatgcaaagaagttt 	ATGAAGAGGTGCTGAGTGACACCTAATGATGGCTTTGCTAAAGTCCATTATGGCTTCA 	CCTGAAGGCACAGAACAAAATTGCTGAGAGCATCCCATATTTAAAGGAAGG	rcctggcactgatgat rcctggcactgatgat	GGGTTGGGAACAAAGAGGCATATAAGTGGTATGAGCTTGGGCACAAGAGAGGACACTTTG 	CTGGCAACGCTCACTC	agaaacgggctacaca 	O1 TCCGAGATGAAGGCCTTGCAGTGATGGATAAAGCCAAAGGTCTCTTCCTGCCTG	GAGGGAAAAAGGGGAC GAGGGAAAAGGGGAC		atgcagaagagacag 	GGCCGCACACAGGGCCCACAAACTGCAGGCTCCGAATGCACCTGGGCCTTGGTGATTCCCA 	aggaaggctgcaagattcgatgtgccaacgagaccaggacctgggaggaaggcaaggtagg 	CATCTTTGATGACTCCTTTGAGCACGAGGTATGGCAGGATGCCTCATCTTTCCGGCTGA 	rcgrgcargrgccar rcgrgcargrgccar	Caatttagcatgaattcatgcaagcttgggaaactctggagaga 2324
aaaatga aaaatga	ATGAAGA ATGAAGA	TCCTGAA TCCTGAA	CCGGAGA CCGGAGA	6667766 666776	CATCTGT CATCTGT	CCCCAAA CCCCAAA	TCCGAGA TCCGAGA	AAAACCT AAAACCT	ATGAAAA ATGAAAA	CAACAGG CAACAGG	GGCCGCA 	AGGAAGG AGGAAGG	TCATCTT 	TATTCAT	CAATTTA CAATTTA
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RESULT 8
US-10-084-817-63
Sequence 63, Application US/10084817
Publication No. US20030119009A1
GENERAL INFORMATION:
APPLICANT: Susan Stuart
APPLICANT: Jed G. Nuchtern

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                                                                                                      241 TTGTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGCTGATGGTGATGGAGAAG
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                                                                                                                                                                        CAGCAGTCCCGCCAGAAGAGGCTGAGCCACACACTGAGCCCGAGGAGCAGGTTCCTGTGG
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                                  GGTTTATGGTGGATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTC
                                                                                                                                                                                                                                 CAGCAGTCCCGCCAGAAGAGGCTGAGCCACACTGAGCCCGAGGAGCAGGTTCCTGTGG
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                                                                                                                                                      ATTITGATGTGGATGATGCCAAAGTTTTATTAGGACTTAAAAGAGAGATCTACTTCAGAGC
GGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC
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                                                                                                                                                                                              2238 CAACAGGATGCAGAAGAGGACAGATCAAATATTCCATCATGATGCACCCCGGGACTCACGTGT
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                                                                                                                                                                            GGCCGCACAGGGCCCACAAACTGCAGGCTCCGAATGCACCTGGGCTTGGTGATTCCCA
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publication No. US20030166887A1

GENERAL INFORMATION:
APPLICANT: The Brigham and Women's Hospital, Inc.
APPLICANT: Yates, Karen
APPLICANT: Mizuno, Shuichi
CURRENT APPLICANTONI UNMBER: US/10/096,534

CURRENT APPLICATION NUMBER: US/10/096,534

CURRENT APPLICATION NUMBER: US 60/274,980

PRIOR FILING DATE: 2001-03-12

NUMBER OF SEQ ID NOS: 79

SOFTWARE: PatentIn version 3.0

SEQ ID NO 37

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99.9%; Pred. No. 0;
live 0; Mismatches
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; ORGANISM: Homo sapiens
US-10-096-534-37
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Best Local Similarity
Matches 945; Conserv
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                                                                                                                                APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Vedrick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Manion, Jane
APPLICANT: Manion, Jane
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Pan, Liqun
APPLICANT: Wang, Aljun
APPLICANT: Wang, Allun
APPLICANT: Wang, A
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; Pred. No. 0;
0; Mismatches
                                                                    ; Sequence 1791, Application US/09736457; Patent No. US20020168637A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.9%;
Matches 690; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
                          RESULT 11
US-09-736-457-1791
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US-09-736-457-1791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GGTTTATGGTGATTGCTGGGCGTCTGGACATCTGTAGCTGTCGTTTGGTTTGATC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 TTGTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGGTGATGGTGATGGAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGCAGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGCAGAAACCCCAGAATATCGAAGATGAAGCAAAAGAAACAAATTCAGTCCCTTCTCCATG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGAACCACAACAAGAGGATGATGAGTTTCTTATGGCGACTGATGTAGATTTG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCATAGTTACCACGTGGAAGAGA 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGITICACAAGACIGIAAICAGGAIAIGGAAGAGAIGAIGICIGAGCAGGAAAAICCAG 720
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                                                                                                                   Length 2680;
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                                                                                                                                                               1;
                                                                                                                   DB 16;
                                                                                                                38.5%; Score 895; DB ilarity 99.9%; Pred. No. 0; Conservative 0; Mismatches
; LENGTH: 2680
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-269-909-3
                                                                                                                                        Similarity
                                                                                                                                        Best Local Simi
Matches 945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199
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281 165 341 225

Gaps

285

461 345 521 641

821

585 761

701

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46 GGAACTTCATTCACGTGGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 GAIGCIGAIGGIGAIGGAGAITITGAIGIGGAIGAGAGAGCCAAAGTITIAITAGGACTIAAA
                                             526 AGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGAAGAGATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTGTCGTTTGGTTTGATCTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 GAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGGCTGAGCCACACTGAGCCC
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                                                                               TCTGAGGAGAAAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCAT
                                                                                                             TCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCAT
                                                                                                                                                    GATACAGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 GGAACTTCATTCACGTGGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTA
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APPLICANT: Fanger, Gary
APPLICANT: Fanger, Gary
APPLICANT: Wang, Aijun
APPLICANT: Wang, Tongtong
APPLICANT: Workell, Particia
APPLICANT: Checker, Anne
APPLICANT: Clapper, Jonathan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121-478C16
CURRENT APPLICATION NUMBER: US/09/849,626
CURRENT PILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 1926
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                              ; Sequence 1791, Application US/09849626; Publication No. US20020197669A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.5%;
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US-09-849-626-1791
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Best Local Simi
Matches 690;
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GATACAGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAA
                  GCTGTCGTTTGGTTTGATCTTGACTATGAGGAAGTTCTAGGAAAACTAGGAATCTAT
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                                                                                                                                                               | Sequence 1791, Application US/09902941
| Sequence 1791, Application US/09902941
| Patent No. US2002172952A1
| GENERAL INFORMATION:
| APPLICANT: Henderson, Robert A. |
| APPLICANT: Wang, Tongtong | APPLICANT: Wang, Tongtong |
| APPLICANT: Waramabe, Yoshihiro | APPLICANT: Warderskis, Margarita |
| APPLICANT: Garter, Marc W. |
| APPLICANT: Marnerakis, Margarita | APPLICANT: Garter, Darrick | |
| APPLICANT: Garter, Darrick | APPLICANT: Catter, Darrick |
| APPLICANT: Catter, Darrick | APPLICANT: Catter, Darria | APPLICANT: Catter, Darria |
| APPLICANT: Bangur, Chaitanya S. |
| APPLICANT: Manbb, Andria |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY |
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER |
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER |
| TITLE PEPERBRUCE: 210121 478617 |
| CURRENT FILING DATE: 2001-07-10 |
| NUMBER OF SEQ ID NOS: 2002 |
| SEQ ID NO 1791 |
| TYPE: NANA
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                                                                                     822 AATGAAGGGATAGAAATCACAGAAGTAACTG 852
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Best Local Similarity 99.9
Matches 690; Conservative
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CORGANISM: Homo sapiens
US-09-902-941-1791
                                                                                                                                                          RESULT 12
US-09-902-941-1791
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Bublication No. US20030170255A1

GBNERAL INPORMATION:

APPLICANT: Watenabb. Yoshihiro

APPLICANT: Henderson, Robert A.

APPLICANT: Alead, Michael D.

APPLICANT: Stath, Paul R.

APPLICANT: Carter, Darrick

APPLICANT: Carter, Darrick

APPLICANT: Carter, Darrick

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121, 478619

CURRENT APPLICATION NUMBER: US/10/113,872

CURRENT FILING DARR: 2002-03-28

NUMBER OF SEQ ID NOS: 2011

SEQ ID NO 1791
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US-10-113-872-1791
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APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Wedvick Thomas S.
APPLICANT: Wedvick Thomas S.
APPLICANT: Wedvick Thomas S.
APPLICANT: Wanbb, Andria
ITTLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
ITTLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REPERBNCE: 210121.478C18
CURRENT FILIAG DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1791
TYPE: DNA
TYPE:
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Sequence 1791, Application US/10017754
Sequence 1791, Application No. US20030054363A1
GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
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Sequence 1791, Application US/10283017
Sequence 1791, Application US/10283017
Seneral INPORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Carter, Durham, Margarita
APPLICANT: Carter, Darrick
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Cary C.
APPLICANT: Panger, Cary C.
APPLICANT: Applicant Seary R.
APPLICANT: And Andria APPLICANT: Mandabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CURRENT APPLICANT: AND SEQ ID NOS: 2157
SOFTWARE: FastSERQ for Windows Version 4.0
SEQ ID NO 1991
LENTH: 2442
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Best Local Similarity 99.9%;
Matches 690; Conservative (
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CRGANISM: Homo sapiens
US-10-283-017-1791
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PREVENTION, AND
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publication No. US20030099974A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: AL, Yongyao

APPLICANT: AL, Yongyao

APPLICANT: AL, Yongyao

APPLICANT: AL, Yongyao

APPLICANT: PERIMAN, Kathleen

TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, FILLE OF INVENTION: THERAPY OF BREAST CANCER

FILE REFERENCE: MRI-049

CURRENT APPLICATION NUMBER: US/10/198,846

CURRENT FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR PILING DATE: 2001-07-18
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
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PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 34279
LENGTH: 502
                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                    452 AAAAGAACAAATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGA 511
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LOCATION: 3009, 3010, 3011, 3012, 3013, 3014, 3015, 3016, 3017, 3018, 2024TION: 3019, 3020, 3021, 3022, 3023, 3024, 3025, 3026, 3027, 3028, 2026, 2027, 3029, 3020, 3031, 3032, 3033, 3034, 3035, 3036, 3037, 3038, 2026, 3037, 3038, 2026, 3037, 3038, 2026, 3037, 3038, 2038, 2039, 3040, 3041, 3042, 3043, 3044, 3045, 3046, 3047, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038, 2038
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US-09-918-995-34279
US-09-918-995-34279
Sequence 34279, Application US/09918995
Publication No.. US20030073623A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT PILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/215,076
                                                                                                                                                                                                                                                                                                                                                       0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.8e-307;
Matches 615; Conservative 0; Mismatches 0;
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                                                                                   344 GCCATCGAGACCTACCAAGAGGTGGCCAGCCTGATGTCCCTGCTGCAGACCTGAGAG
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      Length 502
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APPLICANT: Astle, Jon H.
APPLICANT: Carroll, Eddie III
APPLICANT: Carroll, Eddie III
APPLICANT: Carroll, Bedie III
APPLICANT: Carroll, Bedie III
APPLICANT: Towivedi, Poornima
APPLICANT: Thiagalingam, Arunthathi
APPLICANT: Lewis, Marcia E.
TILLE OF INVENTION: Expressed in Cancer Tissue
FILLE REFERENCE: 1657/1032
CURRENT APPLICATION NUMBER: US/09/969,034
CURRENT APPLICATION NUMBER: 02001-10-02
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 4494
SEQ ID NO 3202
                                         0; Indels
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19.8%; Score 459; DB 10; I
Best Local Similarity 100.0%; Pred. No. 1.7e-226;
Matches 459; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 19
US-09-969-034-3202/c
Sequence 3202, Application US/09969034
Publication No. US20040110668A1
GENERAL INFORMATION:
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251 TGAGGAAGTTCTAGGAAACTAGGAATCTATGATGCTGATGGTGATGGAGATTTTGATGT
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Best Local Similarity 99.7%;
Matches 365; Conservative
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US-10-085-783A-25661
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                                                                                   Query Match 15.4%; Score 359; DB 11; Length 660; Best Local Similarity 100.0%; Pred. No. 1.1e-174; Matches 359; Conservative 0; Mismatches 0; Indels
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13.6%; Score 315; DB 17;
Best Local Similarity 99.7%; Pred. No. 6.4e-152;
Matches 365; Conservative 0; Mismatches 1;
                                        NAME/KEY: misc_feature;

// LOCATION: 507, 554, 599, 656

OTHER INFORMATION: n = A,T,C or G

US-09-969-034-3202
   LENGTH: 660
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                   US-10-242-535A-25661
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US-10-242-535A-25661
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US-10-085-783A-25661
US-10-085-783A-25661
US-10-085-783A-25661
US-10-085-783A-25661
US-10-085-783A-2567
UNUMNITON: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
UURENT APPLICATION NUMBER: US/10/085,783A
UURENT FILING DATE: 2001-02-28
URIOR APPLICATION NUMBER: US 60/205,340
PRIOR PILING DATE: 2001-03-12
PRIOR PILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR PILING DATE: 2001-02-28
UNUMBER OF SEQ ID NOS: 58994
UNUMBER OF SEQ ID NOS: 58994
ULENTH: 366
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                                                  311 GGATGATGCCAAAGTTTTATTAGGACTTAAAGAGAGATCTACTTCAGAGCCAGCAGTCCC
                                                                            371 GCCAGAAGAGGCTGAGCCACACACTGAGCCCGAGGAGCAGGTTCCTGTGGAGGCAGAACC
                                                                                                                                                                                                                 431 CCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATGAAATGGTACA
61 TGAGGAAGTTCTAGGAAAACTAGGAATCTATGATGCTGATGGTGGTGATGGAGATTTTGATGT
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Pred. No. 6.4e-152;
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121 TACACGCAGAACATG 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-2707
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ORGANISM: Human
US-10-085-783A-2707
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                              CGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCACAGGAGAACCACA 550
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                                                                                                                                                                                                                                                                                                               Sequence 2777, Application US/10066543
| Publication No. US20030087918A1
| Publication No. US20030087918A1
| APPLICANT: Jiang Yuqiu
| APPLICANT: Jiang Yuqiu
| APPLICANT: Lodes, Michael J.
| APPLICANT: Lodes, Michael J.
| APPLICANT: Earger, Barrick
| APPLICANT: Seriet, Heacher
| APPLICANT: Seriet, Heacher
| APPLICANT: Sacriet, Heacher
| TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
| TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
| TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 341, 343
SOTHER INFORMATION: n = A,T,C or G
US-10-066-543-277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                             551 ACAAGA 556
                                                                                                                                                                       361 ACAAGA 366
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US-10-242-535A-2707
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APPLICANT: Liew, C.C., Tribe, C.C., C.C., Tribe, C.C., C.C., Tribe, C.C., C
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APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REPERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
FRIOR APPLICATION NUMBER: US 60/305,340
FRIOR APPLICATION NUMBER: US 60/305,017
FRIOR APPLICATION NUMBER: US 60/275,017
FRIOR FILING DATE: 2001-07-13
FRIOR FILING DATE: 2001-07-13
FRIOR FILING DATE: 2001-07-28
NUMBER OF SEQ ID NOS: 58994
SOFFWARE: PARENTLY VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TCCGGCCAGAAGAGGCTGAGCCACACACTGAGCCCGAGGAGCAGGTTCCTGTGGAGGCAG
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US-10-085-783A-2707
US-00-085-783A-2707
Seducation No. US20040037841A1
GENERAL INFORMATION:
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/195,218

PRIOR PILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                         162 GGAACTTCATTCTTCACGTGGTTTATGGTGATTGCATTGCTGGGCGTCTGGACATCTGTA
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Publication No. US20030204075A9
GENERAL INFORMATION
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
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                                                                                                                                                                                                                                                                                                                                                                                  170 GCTGTCGTTTGGTTTGATCTTGTTGACTATGAGAAGTTCTAGG 127
; OIHER INFORMATION: SWISSPROT HIT: Q12797, EVALUE 3.00e-14; OTHER INFORMATION: NT HIT: gil4589865, EVALUE 2.00e-80
US-10-029-386-13264
                                                                                                                                                                                       Indels
                                                                                                                                   4.5%; Score 104; DB 16; 100.0%; Pred. No. 1.3e-42; tive 0; Mismatches 0;
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3.4%; Score 78; DB 13; I
Best Local Similarity 100.0%; Pred. No. 3.7e-29;
Matches 78; Conservative 0; Mismatches 0;
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Publication No. US20020198371A1
GENERAL INFORMATION:
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                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 104; Conservative
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US-10-027-632-2825/c
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SEQ ID NO 2825
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Publication No. US20030194704A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HANDER GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT PILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

LENGTH: 592
                                                                                                                                                                                                                                                                                    Sequence 26644 Application US/10029386
| Publication No. US2030194704A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Penn, Sharron G. APPLICANT: Hanzel, David R. APPLICANT: HONORION: EXPRESSION ANALYSIS TWO FILE REFERENCE: AEONICA-X-2 CURRENT APPLICATION UNMBER: US/10/029,386
| CURRENT APPLICATION UNMBER: 2001-12-20 | NUMBER OF SEQ ID NOS: 34288 | SOFTWARE: Annomax Sequence Listing Engine vers: 1.1 |
| SEQ ID NO 26964 | LENGTH: 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGACATCTGTA 221
                                   61 AACCCCAGAATATCGAAGATGAAGCAAAAAAAAAAAATTCAGTCCCTTCTCCATGAAATGG 120
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.71
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EST_HUMAN HIT: AU132666.1, EVALUE 4.00e-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTHER INFORMATION: MAP TO CHR8.3

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.71

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1

OTHER INFORMATION: SISSEROT HIT: Q12797, EVALUE 4.00e-15

OTHER INFORMATION: EST HUMAN HIT: AW381165.1, EVALUE 9.00e-81

US-10-029-386-26964
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4.5%; Score 104; DB 16; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.2e-42;
Matches 104; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 GCTGTCGTTTGGTTTGATCTTGACTATGAGGAAGTTCTAGG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 GCTGTCGTTTGGTCTTGTTGACTATGAGGAAGTTCTAGG 7
                                                                                                                                                         487 TACACGCAGAACAIG 501
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ORGANISM: Homo sapiens
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US-10-029-386-26964/c
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RESULT 30

1 Sequence 11070 Application US/09908975

2 Sequence 11070 Application US/09908975

3 Fublication No. US20030168843A1

3 GEQUENCE 11070 Application No. US20030168843A1

3 APPLICANT: SHOSHAN, Avi

4 APPLICANT: MASSERMAN, Alon

5 APPLICANT: MINTZ, Eli

5 APPLICANT: MINTZ, List

6 APPLICANT: MINTZ, List

7 TILE OF INVENTION: OLIGONUCLECTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE

7 TILE OF INVENTION: OLIGONUCLECTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS

7 TILE OF INVENTION: OLIGONUCLECTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS

7 TILE OF INVENTION: OLIGONUCLECTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS

7 TILE OF INVENTION: OLIGONUCLECTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS

7 TILE OF INVENTION: OLIGONUCLECTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS

7 TILE OF INVENTION: OLIGONUCLECTION ON TOWNER: US 60/287,724

7 FRICK FILING DATE: 2001-05-02

7 FRICK FILING DATE: 2000-07-28

7 NUMBER OF SEQ ID NOS: 32337

7 SEQ ID NO 11070

7 ENGINE NO 11070

7 ENGINE NO 11070

7 ENGINE NO 11070
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Publication No. US20030211476A1
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Brandon, David
APPLICANT: Brandon, David
APPLICANT: Brandon, David
APPLICANT: Brandon, David
APPLICANT: Happins, Insela
APPLICANT: Happins, Insela
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
FILE REFERENCE: B1067/20087
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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Best Local Similarity 100.0%; Pred. No. 7.3e-20;
Matches 60; Conservative 0; Mismatches 0;
                 293 AGTTTTATTAGG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-11070
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; ORGANISM: Homo sapiens
US-10-116-275-322
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US-10-116-275-322/c
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LENGTH: 2208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.4%; Score 78; DB 17; L
Best Local Similarity 100.0%; Pred. No. 3.7e-29;
Matches 78; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/10443622
Publication No. US20040024192A1
GENERAL INFORMATION:
APLICANT: Carter et al.
TITLE OF INVENTION: 19 Human Secreted Proteins
FILE REFERENCE: P2009P1
CURRENT APPLICATION NUMBER: US/10/443,622
CURRENT APPLICATION NUMBER: US/10/443,622
CURRENT APPLICATION NUMBER: US/00/13/608
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1997-07-01
PRIOR FILING DATE: 1997-07-01
PRIOR PLILING DATE: 1997-07-01
PRIOR APPLICATION NUMBER: 60/051,381
PRIOR PLILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/058,653
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: PARENTH Ver. 2.0
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR RILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-02-28
PRIOR FILING DATE: 1999-02-28
PRIOR FILING DATE: 1999-08-09
NUMBER: PREDICATION NUMBER: US 60/146,002
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASELSEQ FOR WINGOWS VERSION 4.0
SEQ ID NO 2825
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CORGANISM: Homo sapiens
US-10-443-622-24
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; ORGANISM: Human
US-10-027-632-2825
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 Sequence 17, Application US/10755889

Publication No. US20040171823A1

GENERAL INFORMATION:

APPLICANT: Bristol—Myers Squibb Company

TITLE OF INVENTION: PATHWAY

FILE REFERENCE: DO284 NP

CURRENT APPLICATION NUMBER: US/10/755,889

CURRENT PILING DATE: 2004-01-13

PRIOR PILING DATE: 2003-01-14

PRIOR PILING DATE: 2003-01-14

PRIOR PILING DATE: 2003-05-12

NUMBER: OF SEQ ID NOS: 823

SOFTWARE: PatentIn version 3.2

SEQ ID NO 177

LENGTH: 2208
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2.2%; Score 51; DB 11; I
Best Local Similarity 100.0%; Pred. No. 3.7e-15;
Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                    Query Match
2.5%; Score 59; DB 18; I
Best Local Similarity 100.0%; Pred. No. 2.8e-19;
Matches 59; Conservative 0; Mismatches 0;
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i LOCATION: 503, 512, 553, 565, 570, 577, 578
correct INFORMATION: n = A,T,C or G
US-09-969-034-3266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2274 CTTCCAGCAATTTAGCATGAATTCATGCAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3266, Application US/09969034 Publication No. US20040110668A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-10-755-889-177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-969-034-3266/c
US-10-755-889-177/c
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439 CTTCCAGCAATTTAGCATGAATTCATGCAAGCTTGGGAAACTCTGGAGAGA 389

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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 310460
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Best Local Similarity 100.
Matches 39; Conservative
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Matches 39; Conservative
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US-10-027-632-56205/c
                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Human
US-10-027-632-310460
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US-10-027-632-56205
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Publication No. US20020198371A1

GENERAL INFORMATION:

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

FRIOR APPLICATION NUMBER: US 60/18,006

PRIOR PLING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 1990-01-23

PRIOR PLING DATE: 1999-01-23

PRIOR PLING DATE: 1999-01-23

PRIOR FILING DATE: 1999-01-28

PRIOR PRIOR PRIOR DATE: 1999-01-28

PRIOR FILING DATE: 1999-01-28

PRIOR PRIOR PRIOR DATE: 1999-01-28

PRIOR PRIOR PRIOR DATE: 1999-01-28

PRIOR PRIOR PRIOR DATE: 1999-01-28

PRIOR PRIOR DATE: 1990-01-28

PRIOR DATE: 1990-01-28

PRIOR DATE: 1990-0
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APPLICANT: Wang, David G.

ITILE OF INVENTION: Identification and Mapping of Single Nucleotide

ITILE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT PILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR PILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 2000-03-24
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0
                                                                 Query Match
1.9%; Score 44; DB 17; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 44; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 6e-09;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                   304 AGCAGTATATGAACCTCTAGAAATGAAGGGATAGAAATCACAG 347
                                                                                                                                                                                                                               800 AGCAGTATATGAACCTCTAGAAAATGAAGGGATAGAAATCACAG 843
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Sequence 310460, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 39; Conservative
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US-10-027-632-56205/c
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ORGANISM: Human
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US-10-027-632-7020
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US-1U-U27-633-56205/c

Sequence 56205, Application US/10027632

Publication No. US2003020407589

GENERAL INPORMATION:

TITLE OF INVENTION:

TITLE OF INVENTI
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Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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0
     Length 453;
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100.0%; Pred. No. 6e-09;
tive 0; Mismatches 0; Indels
                                                                                                             0; Indels
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1.7%; Score 39; DB 13;
100.0%; Pred. No. 6e-09;
iive 0; Mismatches 0
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Exovalic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: W. Wei
APPLICANT: W. Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Bi, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5)221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 73067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 42949, Application US/10425115
Publication No. US20040214272A1
Fublication No. US20040214272A1
Fublication No. US20040214272A1
Fublication No. US20040214272A1
FublicANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
         TITLE OF INVENTION: NUMBER OF INVENTION: Dlants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 124491
LENGTH: 2135
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100.0%; Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                       DB 18;
1.2;
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US-10-425-115-124491
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Best Local Similarity 100.0%; Pred. No. ...
Matches 21; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1991 GCAGCGCCAACAGCAGCAGCAGC 1969
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Publication No. US20040123343A1
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    Cao, Yongwei
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                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Zea mays
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Matches
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APPLICANT: La Casa Thomas J
APPLICANT: La Casa Thomas J
APPLICANT: Cas Valid David K
APPLICANT: Cas Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRESENCE: 38-21(53233)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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100.0%; Pred. No. 0.36;
tive 0; Mismatches 0; Indels
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US-10-424-599-97119
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Pred. No. 6e-09;
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100.0%; Pred. No. v. o. o. Mismatches
                       CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR PELING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 1000-03-29
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-08-09
PRIOR PILING DATE: 1999-08-09
PRIOR PILING DATE: 1999-08-09
NUMBER OF SEC ID NOS: 325720
SEC ID NO 310460
LENGTH: 453
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-424-599-97119; Sequence 97119, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 24; Conservative
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Best Local Similarity
Matches 39; Conserva
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US-10-425-115-124491/c
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LENGTH: 859
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APPLICANT: Wands, Jack R.
APPLICANT: Deutch, Alan H
APPLICANT: Ge la Monte, Suzanne M
APPLICANT: Ghanbari, Hossein A
ITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REFERENCE: 1486-032 CIP
CURRENT APPLICATION WUMBER: US/09/859,604
CURRENT FILING DATE: 2001-05-17
PRIOR APPLICATION WUMBER: 09/436,184
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence:Location (-6) OTHER INFORMATION: oligonucleotide
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APPLICANT: deal Monte, Suzanne M
APPLICANT: Deutch, Alan H
APPLICANT: Glanbari, Hossein A
TITLE-OF. INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REFERENCE: 21486-032 CIP
CURRENT APPLICATION NUMBER: US/09/859,604
CURRENT FILING DATE: 2001-05-17
PRIOR PPLICATION NUMBER: 09/436,184
NUMBER OF SEQ ID NOS: 13
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37;
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  PRIOR APPLICATION NUMBER: 09/436,184
PRIOR FILING DATE: 1999-111-08
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 20
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US-09-859-604-11/C
US-09-859-604-11/C
Sequence 11, Application US/09859604
Patent No. US20020110559A1
GENERAL INFORMATION.
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US-09-859-604-12/c
; Sequence 12, Application US/09859604
; Patent No. US20020110559A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          11 AATGGCCCAGCGTAAGAATG 30
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                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
FEATURE:
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US-10-308-503-188

Sequence 188, Application US/10308503

Publication No. US20030191080A1

GENERAL INFORMATION:

APPLICANT: PHILLIPS, M. IAN

TITLE OF INVENTION: ANTIENBE COMPOSITIONS TARGETED TO BETAL-ADRENOCEPTOR-SPECIFIC MR

TITLE OF INVENTION: MATHERNE COMPOSITIONS TARGETED TO BETAL-ADRENOCEPTOR-SPECIFIC MR

TITLE OF INVENTION: MATHERNE US/10/308,503

CURRENT FILING DATE: 2003-12-03

FRIOR APPLICATION NUMBER: US/10/308,503

CURRENT FILING DATE: 2000-07-11

PRIOR FILING DATE: 1998-09-14

PRIOR FILING DATE: 1998-09-14

SRIOR APPLICATION NUMBER: 09/152,717

PRIOR FILING DATE: 1998-09-14

NUMBER OF SEQ ID NOS: 204

SEQ ID NOS: 204

SEQ ID NOS: 204

SEQ ID NOS: 204

LENGTH: 1445
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APPLICANT: de la Monte, Suzanne M
APPLICANT: Deutch, Alan H
APPLICANT: Ghanbari, Hossein A
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REPERENCE: 21486-032 CIP
CURRENT APPLICATION NUMBER: US/09/859,604
CURRENT FILING DATE: 2001-05-17
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                                                                                                                                                                                                                                    Query Match 0.9%; Score 21; DB 18; Length 715; Best Local Similarity 100.0%; Pred. No. 13; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                 ; OTHER INFORMATION: Clone ID: MRT4577_139178C.1
US-10-425-115-42949
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LOCATION: (1828)...(1828)
LOCHER INFORMATION: WHERE N = A, T, C OR G
US-10-308-503-188
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; Sequence 10, Application US/09859604
; Patent No. US20020110559A1
; GENERAL INFORMATION:
CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 369326 SEQ ID NO 42949 LENGTH: 715
                                                                                              TYPE: DNA
ORGANISM: Zea mays
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Best Local S
Matches 21
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TYPE: DNA ORGANISM: Glycine max
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPRENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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COTHER INFORMATION: Description of Artificial Sequence:Locations (-11)
COTHER INFORMATION: 01190nucleotide
US-09-859-604-12
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100.0%; Pred. No. 40;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match . 0.9%; Score 20; DB 9; Length 20; Best Local Similarity 100.0%; Pred. No. 37; Matches 20; Conservative 0; Mismatches 0; Indels
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US-10-425-115-22449
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US-10-425-115-21348
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                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Zea maye
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ORGANISM: Zea mays
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US-10-425-115-21348/c
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LENGTH: 183
                                            SEQ ID NO 12
LENGTH: 20
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Sequence 89196, Application US/10424599
Sequence 89196, Application US/10424599
Sequence 89196, Application No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
TITLE OF INVENTION: SOy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 89196
LENGTH: 495
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kovalic, David K.
APPLICANT: Applicant: Vihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REPERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 26002
LENGTH: 489
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US-10-424-599-89196
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LOCATION: (1)..(495)
OTHER INFORMATION: unsure at all n locations
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  Query Match 0.9%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 41; Matches 20; Conservative 0; Mismatches
Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                  US-10-767-701-26002/c
US-10-767-701-26002/c
US-10-767-701
US-10-76
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US-10-767-701-26002
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Sequence 3202022/C

Sequence 3202022/Application US/10027632

Publication No. UG30020198371A1

GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR PILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 1000-03-24

PRIOR FILING DATE: 1000-03-24

PRIOR FILING DATE: 1099-11-23

PRIOR FILING DATE: 1099-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-11-23

PRIOR PRILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-11-23

PRIOR PRILING DATE: 1999-11-23

PRIOR PRILING DATE: 1999-00-05

PRIOR PRINCE PRINCE PRINCE PRINCE PRINCED DATE: 1999-00-05

PRINCE PRINCED DATE: 1999-00-05

PRINCE PRINCED DATE: 1999-00-05

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US-10-027-632-322023/c

Sequence 322023, Application US/10027632

Publication No. US2020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REPERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

FRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PILING DATE: 2000-04-20

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-24
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100.0%; Pred. No. 42;
.ive 0; Mismatches 0; Indels
                                                                                  DB 13; Length 567; 42;
                                                                                                                                             0; Indels
                                                                                  Query Match 0.9%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 42; Matches 20; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                             212 GAACAAAAGCAAAAGTTAA 193
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Best Local Similarity 100.
Matches 20; Conservative
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US-10-027-632-322022/c
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; ORGANISM: Human
US-10-027-632-322022
   ; ORGANISM: Human
US-10-027-632-82527
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                                                                                                                                   Sequence 9144, Application US/10029386
Sequence 9144, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR OF TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SSEQ ID NO 9144
LENGTH: 550
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GOTHER INPORMATION: MAP TO AC007262.4
GOTHER INPORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
OTHER INPORMATION: EXPRESSED IN BEALN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: SMISSPROT HIT: P54258, EVALUE 1.80e+00
OTHER INFORMATION: MT HIT: AB051488.1, EVALUE 0.00e+00
OTHER INFORMATION: EST_HUMAN HIT: B1458804.1, EVALUE 7.00e-63
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402 AGAAAAGAAGCCTAAACTT 421
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ORGANISM: Homo sapiens
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US-10-027-632-82527/c
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APPLICANT: Wanstlow:
APPLICANT: Wanstlow:
APPLICANT: Wanstlow:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: DOLYMORPHISMS in the Human Genome
FILE REFERENCE: 108827.129
CURRENT PLING DATE: 2002-04-30
FRIOR PILING DATE: 2002-04-30
PRIOR PLING DATE: 2000-07-12
PRIOR PLING DATE: 2000-07-12
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-02-44
PRIOR PLING DATE: 1900-02-44
PRIOR PLING DATE: 1900-02-44
PRIOR PLING DATE: 1909-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-08
NUMBER OF SEQ ID NOS: 325720
SOFTWARE FRIENG DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
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42;
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42;
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100.0%; Pred. No. -...
                  CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR PELING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PLILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR PILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR PLILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PRESEED FOR WINDOWS Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20;
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Best Local Similarity 100.0%; P:
Matches 20; Conservative 0;
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Best Local Similarity 100.
Matches 20; Conservative
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US-10-027-632-322022
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US-10-027-632-322023
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LENGTH: 567
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION WUMBER: US 60/218,006
FRIOR APPLICATION NUMBER: US 60/218,006
FRIOR PELING DATE: 2000-07-12
FRIOR PELING DATE: 2000-07-22
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-09-08-08
FRIOR FILING DATE: 1999-09-08-08
FRIOR FILING DATE: 1999-09-08-08
FRIOR FILING DATE: 1999-08-08
FRIOR FILING DATE: 1999-08-08
FRIOR APPLICATION NUMBER: US 60/146,002
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                                                                                                                                                                                                                                                                                                                                                                                                              0.9%; Score 20; DB 13; Length 567; 100.0%; Pred. No. 42;
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100.0%; Pred. No. 42;
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ive 0; Mismatches
PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FRACESEQ FOR Windows Version 4.0

SEQ ID NO 322023

LENGTH: 567
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Publication No. US20030204075A9
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 20; Conservative
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Matches 20; Conserv
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US-10-027-632-322022/c
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US-10-027-632-82527/c
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ORGANISM: Human
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ORGANISM: Human
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; Sequence 1, Application US/10822613
; Publication No. US2005002905A1
; GENERAL INFORMATION:
JERNETAL INFORMATION:
TO SEPLICANT: SCARPACE, PHILIP J.
APPLICANT: SCARPACE, PHILIP J.
APPLICANT: LI, GANG
TITLE OF INVENTION: OF USE
TITLE OF INVENTION: OF USE
FILE REPERENCE: 4300.01540
CURRENT APPLICATION NUMBER: US/10/822,613
CURRENT FILING DATE: 2004-04-12
FRIOR PELICATION NUMBER: 60/462,496
FRIOR FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 54
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 1
LENGTH: 804
TYPE: DNA
CORDANISM: Homo sapiens
US-10-822-613-1
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBACE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 24406
LENGTH: 843
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US-10-437-963-24406
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yinua
APPLICANT: Cao, Yongwei
APPLICANT: Wwi
APPLICANT: Barbaruk, Brad
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
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ORGANISM: Oryza sativa
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Sequence 71261, Application US/10437963
Fublication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Brabazuk, Brad
APPLICANT: B
                                                                                                                                                                        Sequence 112661, Application US/10425115
Publication Wo. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-4-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NOS: 369326
SEQ ID NOS: 369326
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US-10-437-963-71261
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US-10-425-115-112661
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               212 GAACAAAAGCAAAAGTTAA 193
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ORGANISM: Oryza sativa
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ORGANISM: Zea mays
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US-10-822-613-1
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Suppression of the NURR
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Applicant: Active the construction of the const
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 105. Application US/09853386
; Sequence 105. Application US/09853386
; Patent No. US20020049151A1
; GENERAL INFORMATION:
    APPLICANT: Murphy, Evelyn
; APPLICANT: Bresnihan, Barry
; APPLICANT: Conneely, Orla
    APPLICANT: Fitzgerald, Oliver
; TITLE OF INVENTION: Thorspetuic Approaches to Diseases by Suppressi;
    TITLE OF INVENTION: Thorspetuic Approaches
; TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors
; FILE REFERENCE: PO1972US1
; CURRENT APPLICATION NUMBER: US 60/203645
; CURRENT FILING DATE: 2000-05-11
; FRIOR APPLICATION NUMBER: US 60/203645
; RINDRER OF SEQ ID NOS: 133
; SOFTHARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·,
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.00.0%; Pred. No. 43;
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US-10-425-115-180542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Human Genome Sciences, Inc. et al.
TITLE OF INVENTION: 95 Human secreted proteins
FILE REFERENCE: PZ027P1
CURRENT APPLICATION NUMBER: US/09/397,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)..(1011)
OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Prea. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-397-945-80/c
; Sequence 80, Application US/09397945
; Publication No. US20030065139A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 20; Conservative
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Best Local Similarity 100.
Matches 20; Conservative
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; ORGANISM: HUMAN
US-09-853-386-105
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                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Fing
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5)3221)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 51503
LENGTH: 924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: Clone ID: PAT_MRT4530_53889C.1
US-10-437-963-51503
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APPLICANT: WITTIG, Burghardt
APPLICANT: STEIN, Christoph
APPLICANT: STEIN, Christoph
APPLICANT: SCHARFER, Michael
APPLICANT: SCHARFER, Matthiael
APPLICANT: SCHROFF, Matthiael
APPLICANT: JUNGHANS, Claas
APPLICANT: JUNGHANS, Claas
APPLICANT: WOENIG MEREDIZ, Sven A.
TITLE REFERENCE: WHL-NP-A3
CURRENT APPLICATION NUMBER: 2003-08-22
RIOR APPLICATION NUMBER: DE 101 09 092.7
PRIOR APPLICATION NUMBER: PCT/DE02/00583
PRIOR APPLICATION NUMBER: PCT/DE02/00583
PRIOR APPLICATION NUMBER: PCT/DE02/00583
PRIOR FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 936
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LOCATION: (847)...(933)
OTHER INFORMATION: beta-endorphin cDNA sequence
US-10-646-620A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 180542, Application US/10425115
Publication No. US20040214272A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/10646620A Publication No. US20040138115A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401 GCAACAGCAGCAGCAGCGGC 420
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              Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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              APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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RESULT.

Sequence 37, Application US/10287971

Sequence 37, Application US/10287971

Publication No. US20040067882A1

Publication No. US20040067882A1

SERENT APPLICANT: ALGODONOK, et al

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

FILE REFERENCE: 21402-460A

CURRENT APPLICATION NUMBER: US/10/287,971

CURRENT FILING DATE: 2002-11-05

PRIOR PILING DATE: 2001-11-29

PRIOR PELING DATE: 2001-11-29

PRIOR PELING DATE: 2001-11-05

PRIOR PELING DATE: 2001-11-05

PRIOR PELING DATE: 2001-10-05

PRIOR PELING DATE: 2001-11-06

PRIOR PELING DATE: 2001-11-09

PRIOR PELING DATE: 2001-11-09
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US-09-560-288-1
US-09-560-288-1
US-09-560-288-1
Sequence 1, Application US/09960288
Patent No. USZ0020064833A1
GENERAL INFORMATION:
APPLICANT: Fagerlund, Tore
APPLICANT: Alestron, Peter
APPLICANT: Alestron, Recombinant plasmids and method for treating substance abuse
FILE REFERENCE: 406801
CURRENT APPLICATION NUMBER: US/09/960,288
CURRENT FILING DAFE: 1999-10-26
FRICK FILICATION NUMBER: 09/426,877
PRIOR FILICATION NUMBER: 09/426,877
PRIOR FILICATION NUMBER: 09/426,877
PRIOR FILICATION NUMBER: 09/426,877
SEQ ID NOS: 2
SOUTHARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 1230
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           PRIOR FILING DATE: 1998-03-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 40.0
; SOFTWARE: PatentIn Ver. 2.0
; SOFTWARE: PatentIn Ver. 2.0
; SOFTWARE: PatentIn Ver. 3.0
; LENGTH: 1109
; TYPE: DDA
; TYPE: DDA
; ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.9%; Score 20; DB 9; Length 1230; Best Local Similarity 100.0%; Pred. No. 43; Matches 20; Conservative 0; Mismatches 0; Indels
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CRGANISM: Homo sapiens
US-09-960-288-1
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Publication No. US20040048304A1

Publication No. US20040048304A1

APPLICANT: Ruben et. al.

ITILE OF INVENTATION: 95 Human secreted proteins
FILE SPETICANT: PROBLEM STATE OF TOWN 
CURRENT FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-03-18
PRIOR PELICATION NUMBER: 60/078,56
PRIOR PELICATION NUMBER: 60/078,56
PRIOR PELICATION NUMBER: 60/078,57
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
PRIOR PELICATION NUMBER: 60/078,579
PRIOR PELICATION NUMBER: 60/078,579
PRIOR PELICATION NUMBER: 60/078,579
PRIOR PELICATION NUMBER: 60/080,314
PRIOR PELICATION NUMBER: 60/080,314
PRIOR PELICATION NUMBER: 60/080,314
PRIOR PELICATION NUMBER: 60/080,312
PRIOR PELICATION NUMBER: 60/078,578
PRIOR PELICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-03-19
PRIOR PELICATION NUMBER: 60/078,571
PRIOR PELICATION NUMBER: 60/078,573
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CRGANISM: Homo sapiens
US-09-397-945-80
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US-10-653-595-80/c
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TYPE: DNA
ORGANISM: Homo sapiens
US-10-913-196-2
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Best Local Similarity
Matches 20; Conserv
                                 TYPE: DNA
ORGANISM: Zea mays
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           LENGTH: 1435
                                                                                FEATURE:
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APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Solou, Yihua

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Co., Yongwin

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: WINDER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114
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Sequence 19062, Application US/10425115

FUBLication No. US20040214272A1

FUBLICANT: La Rosa, Thomas J.

APPLICANT: Each State Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 19062
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US-10-425-114-23644
PRIOR FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: 60/406,181
PRIOR FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 397
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 37
LENGTH: 1245
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23644, Application US/10425114 Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 GCAACAGCAGCAGCAGCGGC 119
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                                                                                                                                                                                     ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (90)..(1091)
US-10-287-971-37
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Best Local Similarity
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LENGTH: 1282
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APPLICANT: LIE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
APPLICANT: Pastan, Ira H.
APPLICANT: Baland, Kristi
APPLICANT: Ee- Byungkook
APPLICANT: Vincent, James
ITLEOF INVENTION: GENE EXPRESSED IN BREAST CANCER AND METHODS OF USE
FILE REFERENCE: 4239-66345-02
CURRENT FILING DATE: 2004-08-05
PRIOR PILING DATE: 2003-08-08
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.2
LENGTH.
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
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100.0%; Pred. No. 43;
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; OTHER INFORMATION: Clone ID: MRT4577_117387C.1
US-10-425-115-19062
                                                                          Query Match 0.9%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 43; Matches 20; Conservative 0; Mismatches
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Conservative 0; Mismatches
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Publication No. US20040034888A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10913196
Publication No. US20050053988A1
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0.9%; Score 20; DB 17; Length 1891;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels (
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; FEATURE:
; NAME/KEY: CDS
: LOCATION: (193)..(1380)
; OTHER INFORMATION:
US-10-310-154-280
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FULE REFERENCE: 38-15(52796)B
CURRENT PELICATION NUMBER: 08/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 280
LENGTH: 1891
LYPE: DNA
ORGANISM: Oryza sativa
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; OTHER INFORMATION: Clone ID: UC-ZMFLMO17307H04_FLI US-10-425-114-34740
                                                                                                                                                                                                                                                                                                                                                                                                            US-10-310-154-280
US-10-154-280
US-10-154-280
Publication No. US20030233670A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
APPLICANT: Chomet, Paul S.
APPLICANT: Adams, Thomas H
APPLICANT: Adams, Thomas H
APPLICANT: Adams, James A.
APPLICANT: Ball, James A.
APPLICANT: Ball, Garea A.
APPLICANT: Ball, Sanu, G.
APPLICANT: Bell, Exin
APPLICANT: Bell, Stephan M.
APPLICANT: Bell, Stephan M.
APPLICANT: Huang, Shibshieh
APPLICANT: Huang, Shibshieh
APPLICANT: Lacetti, Lucille B.
APPLICANT: Malson, Linda L.
APPLICANT: Malson, Linda L.
APPLICANT: Manchikanti
APPLICANT: Parmesen, Dan
APPLICANT: Parmesen, Dan
APPLICANT: Tennesen, Dan
APPLICANT: Tennesen, Dan
APPLICANT: Wang, Haiyun
APPLICANT: Wang, Haiyun
APPLICANT: Wang, Haiyun
APPLICANT: Wang, Chunchi,
APPLICANT: Wang, Chunchi,
APPLICANT: Wang, Chunchi,
APPLICANT: Zhang, Qiang
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Sequence 14996, A Sequence 11878, A Sequence 13554, A Sequence 17029, A Sequence 17762, A Sequence 157762, A	Sequence 3520 Sequence 1346 Sequence 6183 Sequence 4400	Sequence 179 Sequence 25, Sequence 110, Sequence 5583	Sequence 49, Sequence 264, Sequence 2642	Sequence 633, Sequence 1353	Sequence 123 Sequence 1436 Sequence 1561	Sequence 1733 Sequence 1735	Sequence 1456	Sequence 1711 Sequence 1277	Sequence 13, Sequence 3024 Sequence 2, 7	Sequence 1060 Sequence 1040 Sequence 4. 7	Sequence 1689	Sequence 3636 Sequence 4042	Sequence 4213 Sequence 4213	Sequence 4213 Sequence 4213	Sequence 4214 Sequence 5313	Sequence 6730 Sequence 6941	Sequence 6941 Sequence 6941	Sequence 7991 Sequence 7991	Sequence 7991	Sequence 1133	Sequence	Sequence	Sequence 1	Sequence	Sequence	Sequence 1 Sequence 2	Sequence 1	Sequence	Sequence 1 Sequence 1	Sequence	Sequence 3	
4 US-09-949-016-14996 4 US-09-949-016-11878 4 US-09-949-016-13554 4 US-09-949-016-17029 4 US-09-949-016-12762 4 US-09-949-016-12762	S S S S S	s is is is	S S S S	s s		is is	S S	Sin Si	S S S	Sh is	Sn	SSS	is is	ns ns	is n	s is	ds ds	s is	is is	SD S	Sn	SS	ŝ	- as	SD:	ds ds	-sn	ns	s s	ns.	ns.	
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GenCore version 5.1.6 t (c) 1993 - 2005 Compugen h, using sw model	2005, 17:12:50 ; Search time (without ali 9320.361 Mil	:-09-436-184-3 24 cggaccgtgcaatggcccagcttggga	, Gapext 60.0	qs, 818138359 residues		sfying chosen parameters:	0 2000000000		tents_NA:* 6/ptodata/1/ina/5A_COMB.seq:*	<pre>gn2_6/ptodata/1/ina/5B_COMB.seq:* gn2_6/ptodata/1/ina/6A_COMB.seq:* gn2_6/ptodata/1/ina/6B_COMB.seq:*</pre>	6/ptodata/1/ina/PCTUS_COMB_seq 6/ptodata/1/ina/backfiles1_seq	ber of results predicted by c	qual to the score of t sis of the total score	SUMMARIES		an !	44	4 4	4 W	4 4	4 US-09-671-325-17	4 US-09-949-016-1	4 US-09-949-016-1	44	4 US-09-949-016-2	4 4	4 US-09-614-034-18 4 US-09-859-604-10	4 .	4 US-09-859-604-12 4 US-09-621-976-24	4 US-09-489-039A-1 4 US-09-949-016-13		•
Copyright:	March 25,	US-09-436- core: 2324 1 cggaccgt	table: OLIGO_NUC Gapop_60.0	1202784 seqs	0	of hits sa	seg length: seg length:	essing: Listing f	Issue 1: /c	2: /cgn2 3: /cgn2 4: /cgn2	0.0	No. is the	greater tha		Query	core march Le	100.0	324 100.0 324 100.0	324 100.0 785 33.8	27.5	27.5	0.0	. 60	3.3 1.1	5.5	0.0 0.0	o.o	6.0	200	o. o.		
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GCTCCGGCAGCGGTAGCACAGTGCGGGCAGCAGCAGCCCCGGGGGCCCCGGAGAGAAA 120
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                                                                                                                                    APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
APPLICANT: de la Monte, Suzanne M.
APPLICANT: Carlson, Rolf I.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REPERENCE: 21466-032 DIVS,
CURRENT APPLICATION NUMBER: US/09/903,248
CURRENT FILING DATE: 2001-07-11
PRIOR PPLICATION NUMBER: 09/436,184
PRIOR PPLICATION NUMBER: 09/436,184
PRIOR PPLICATION NUMBER: 09/436,184

SOFTWARE PRECED NOS: 9
SOFTWARE PRECED NOS: 9
LENGTH: 2324
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ALIGNMENTS
                                                                                Sequence 3, Application US/09903248; Patent No. 6783758; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 2324; Conservative
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CORGANISM: Homo sapiens
US-09-903-248-3
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අු	61 CAGATGATCCAGAACAAAAGCAAAAGTTAAGAAAAAAAGAAG	102
8	1021 ITGATAAGACTATTAAAGCTGAACTTGATGCTGCAGAAAAACTCCGTAA	CTCCGTAAAAGGGGAAAAA 1080
а С	ZI TTGATAAGACIATTAAAGCIGAACIIGAIGCIGCAGAAAAA	7
δλ	1 TIGAGGAAGCAGIGAAIGC	3TCCACGAG 11
qq	81 TTGAGGAAGCAGTGAATTTAAAGAACTAGTACGCAAATACCCT	srccaccac 11
δλ	1141 CAAGATATGGGAAGGCGCAGTGTGAGGATGATTGGCTGAGAAGAGGAGAAAAAAAA	STAATGAGG 12
Ор	11 CAAGATATGGGAAGGCGCAGTGTGAGAATGATTTGGCTGAGAA	staatsass 12
δλ		CCTGCAG 12
QQ	1201 factaceredadecarceadacetaceadadageceagecrace	drocordoad 1260
δλ	1261 ACCTGCTGAAGCTGAATTTGAAGCGTCGCTCAGACAGCCAACAATTCT	GGTCATATGA 1320
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۵,	1321 GAGGITCCCIGCITACCCIGCAGAGAITAGITCAACIAITICCCAAIGA	PACTICCITAA 1380
QQ	1321 GAGGÍTCCCÍGCTÍACCCÍGCAGAGATTAGITCAACTAITTCCCAAIGA	ACTICCITAA 1380
ò	1381 AAAATGACCTTGGCGTGGGATACCTCTTGATAGGAGATAATGACAATGC	AAGAAAGTTT 1440
Д	1381 AAAATGACCTTGGCGTGGGATACCTCTTGATAGGAGATAATGACAATGC	AAGAAAGTTT 1440
ò	1441 ATGAAGGGGCCTGAGTGTGACACCTAATGATGCTTTGCTAAAGTCCA	TATGGCTTCA 1500
. · qq	. 1441 Argandadoriociónoriorocarocianto arocitada de contra de con	rrardcrica 1500
λ	1501 TCCTGAAGGGACAGAACAAAATTGCTGAGAGCATCCCATATTTAAAGGA	AGGAATAGAAT 1560
QΩ	1501 TCCTGAAGGCACAGAACAAATTGCTGAGAGCATCCCATATTTAAAGGA	dgaaragaar 1560
δλ	1561 CCGGAGATCCTCGCACTGATGATGGAGAGATTTATTTCCACCTGGGGGA	
ΩÞ	1561 ccgcActccrcgcActcArcarcacatrtratrtccAccrcgcga	reccarecada 1620
λ	1621 GGGTTGGGAACAAAGAGGCATATAAGTGGTATGAGCTTGGGCACAAGAC	AGGACACTTTG 1680
qq	1621 GGGTTGGGAACAAAGAGGCATATAAGTGGTATGAGCTTGGGCACAAGAC	AGGACACTTTG 1680
λ	1681 CATCTGTCTGGGAACGCTCACTCTACAATGTGAATGGACTGAAAGCACAGCCTTGGTGGA 174	SCCTTGGTGGA 1740

	RESULT 3 US-09-903-216-3 ; Sequence 3, Application US/09903216 ; Patent No. 6812206 ; GENERAL INFORMATION: ; APPLICANT: Wands, Jack R. ; APPLICANT: de la Monte, Suzanne M.	; APPLICANT: Ince, Ned1m; APPLICANT: TICE, Ned1m; APPLICANT: Carlson, FOLD I. ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS; FILE REFERENCE: 21486-032 DIV2; CURRENT APPLICATION NUMBER: US/09/903,216; CURRENT FILING DATE: 2001-07-11; PRIOR APPLICATION NUMBER: 09/436,184; PRIOR FILING DATE: 1999-11-08	; NUMBER OF SEQ ID NOS: 9 ; SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 3 ; LENGTH: 2324 ; TYPE: DNA ; ORGANISM: Homo sapiens UIS-09-903-216-3	Query Match Best Local Similarity 100.0%; Score 2324; DB 4; Length 2324; Best Local Similarity 100.0%; Pred. No. 0; Matches 2324; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Oy 1 CGGACCGGCAGCCAGCGTAAGAATGCCAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA	1 CGGACCGTGCATGACCGTAAGAATGCCAAGAGCACGGCAACAGCAGCAGCAGCAGCAGCAGCAG	Qy 121 AGCATGGAGGACACAAGAATGGGAGGACAGCTCTCGGGAACTTCTTCACGT 180 Db 121 AGCATGGAGGACACACAAGAATGGGAGGAGAACTCTCGGGAACTTCTTCACGT 180 Oy 181 GGTTTAGGTTGCATTGCTGGACATCTGGACATCTGTAGGTTTGGTTTGATC 240	181 GGTTTATGGTGATTGCTGGGCGTCTGGGCATCTGTAGCTGTGGTTTGGTTTGATCTGTTTGGTTTGATCTGTGAGGTGTGTGT	OY 301 ATTTGATGTGGATGATGCCAAAGTTTATTAGGACAGAGAGAG	421 AGCAGAACCCCAGAATATCGAAGATGAAGCAAAACAACAAATTCAGTCCCTTCTCCATG 	Oy 481 AAATGGTACACGCAGAACATGTTGAGGGAGAACATTGCAACAAGAAGACGTCGACCCACAG 540
Qy 1141 CAAGATATGGGAAGGCGCAGTGTGAGGATGATTTGGCTGAGAAGAAGAAGTAATGAGG 1200 Db 1141 CAAGATATGGGAAGGCGCAGTGTGAGTTTGGCTGAGAAGAAGTAATATGAGG 1200 Qy 1201 TGCTACGGAGCCATCCAACCAAGAGGGGCCAGCCTACCTGAGG 1260 Db 1201 TGCTACGGAGCCATCGAGACTACCAAGAGGTGGCCAGCCTACCTGATGTCCCTGAGG 1260 DD 1201 TGCTACGTGGAGCCATCGAGACCTACCAAGAGGTGGCCAGCCTACCTGATGTCCCTGATGTCCTTGAGG 1260	1261 ACCTGCTGAAGCTGAGTTTGAAGCGTCGCTCAGACAACTATTCTAGGTCATATGA 1320	Qy 1381 AAAATGACCTTGGCGTGGGATACCTCTTGATAGGAGATATGCAAAGAAGTTT 1440 Db	01 01 61	.O Q—0	OY 1681 CATCTGTCTGGCAACGCTCACTCTACAATGTGAATGGACTGAAAGCACCAGCTTGGTGGA 1740 1681 CATCTGTCTGGCAACGCTCACTCTACAATGTGAATGGACTGAAAGCACAGCCTTGGTGGA 1740 OY 1741 CCCCAAAAGAAACGGCTACACAGAGTTAGTAAAGTCTTTAGAAAGAA	1801 TCCGAGATGAAGGCCTTGCAGTGATAAAGCCAAAGGTCTCTTCCTGCCTG	192 198 198	Qy 1981 CAACAGGATGCAGAAGAGGACAGATCAAATATTCCATGCACCCCGGGACTCACGTGT 2040 .	accacacacacacaccacaaactacaagactccaaatacactaga agaaggctccaagattcgatgtgccaacgagaccaggacctggg 	2161 TCATCTTTGATGACTCC

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AAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAACAAGAAGATGGACCCCACAG 540 GAGAACCACAACAACAAGGATGATGATTTCTTATGGCGACTGATGATGATGATAGATTTG 600	oy D	1621 GGGTTGGGAACAAAGAGGCATATAAGTGGTATCAGCTTGGGCACAAGAGAGAG
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TAAAT	Qy Dp	2041 GGCCGCACACAGGCCCCACAAACTGCAGGCTCCGAATGCACCTGGGCTTGGTGATTCCCA 2100 2041 GGCCGCACACAGGGCCCACAAACTGCAGGCTCCGAATGCACCTGGGCTTGGTGATTCCCA 2100
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FILING DATE: 17-MAR-1998
CLASSIFICATION: 530
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     GGGTTGGGAACAAGAGGCATATAAGTGGTATGAGCTTGGGCACAAGAGAGGACACTTTG
                                                                                                                 CATCTGTCTGGCAACGCTCACTCTACAATGTGAATGGACTGAAAGCACAGCCTTGGTGGA
                                                                                                                                                                CATCTGTCTGGCAACGCTCACTCTACAATGTGAATGGACTGAAAGCACAGCCTTGGTGGA
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; Patent No. 6166176
; GENERAL INFORMATION:
APPLICANT: Radosevich, James A.
TITLE OF INVENTION: CANCER
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
STREET: Chicago
CITY: Chicago
STATE: Illinois
COUNTY: USA
COUNTY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIEN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,485
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                                                                         226 GAGAGATCTACTTCAGAGCCAGCAGTCCCGCCAGAAGAGGCTGAGGCCACACACTGAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGGAGCAGGTTCCTGTGGAGGCAGAACCCCCAGAATATCGAAGATGAAGCAAAAGAACAA
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GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Carter, Tom
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Ranion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Pan, Liqun
APPLICANT: 1000: CARPOSITIONS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT FILLON NUMBER: US/09/736,457
CURRENT FILLON NUMBER: US/09/736,457
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1791
LENGTH: AA42
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                                                                                                                                                                                                                                                                               822 AATGAAGGGATAGAAATCACAGAAGTAACTG 852
                                                                                                                                                                                                                                                                                                           706 AATGAAGGGATAGAAATCACAGAAGTAACTG 736
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Sequence 1791, Application US/09736457
Patent No. 6509448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA; ORGANISM: Homo sapiens
US-09-736-457-1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Patent No. 6509448
; GENERAL INFORMATION:
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                                 766 TCACAGGTAATTGTAGAAGAAGTAAGCATTTTTCCTGTGGAAGAACAGCAGGAAGTACCA 825
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        TCACAGGTAATTGTAGAAGAAGTAAGCATTTTTCCTGTGGAAGAACAGCAGGAAGTACCA 941
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Pred. No. 3e-297;
0; Mismatches 1; Indels
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bengur, Chaitanya S.
APPLICANT: Lodes, Micheel A.
APPLICANT: Garger, Gary
APPLICANT: Vedvick, Ton
APPLICANT: Retter, Darrick
APPLICANT: Marc
APPLICANT: Marc
APPLICANT: Mannion, Jane
APPLICANT: Pan, Lidun
APPLICANT: APPLICANTON: COMPOSITIONS AND METHODS FOR
ITLE OF INVENTION: DAMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 20121, 478G14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT APPLICATION NUMBER: US/09-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSEQ for Windows Version 3.0
TEACH OF TAXABLE OF TA
                                                                                                                                                                                                                                                                       Sequence 1791, Application US/09702705
Patent No. 6504010
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 27.5%;
Best Local Similarity 99.9%;
Matches 690; Conservative
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; ORGANISM: Homo sapiens
US-09-702-705-1791
                                                                                                     942 CCAGA 946
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826 CCAGA
                                                                                                                                                                                                                            RESULT 7
US-09-702-705-1791
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286 GAGGAGCAGGTTCCTGTGGAGGCAGAACCCCCAGAATATCGAAGATGAAGCAAAAGAACAA 345
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                                                                                                                              GATGTAGATGATAGATTTGAGACCCTGGAACTTGAAGTATCTCATGAAGAAACGGAGCAT
                                                                                                                                                                                                                                                     642 AGTTACCACGTGGAAGACAGATTTCACAAGACTGTAATCAGGATATGGAAGATGATG
                                                                                                                                                                                                                                                                        586 TCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGAAGAAGAAGAAGATGCACAT
                                                                                                                                                                                                                                                                                                                                                                                                                              646 GATACAGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAA
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                                                                        346 ATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAGACACTTGCAA
                                                                                                           CAAGAAGATGGACCCACAGGAACCACACAAGAGGATGATGAGTTTCTTATGGCGACT
                                                                                                                                                                                GATGTAGATGATAGATTTGAGACCCTGGAACCTGAAGTATCTCATGAAGAAACCGAGCAT
                                                                                                                                                                                                                                                                                                                        702 TCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGAAGATGAAAGATTGCACCAT
                                                                                                                                                                                                                                                                                                                                                                                               GATACAGATGATGTAACATACCAAGTCTATGAGGAACAAGCAGTATATGAACCTCTAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09659521
; Sequence 1, Application US/09659521
; Patent No. 6727080
; GENERAL INPORMATION:
; APPLICANT: RADOSEVICH, JAMES A.
; TITLE OF INVENTION: GENE ENCODING LABYRINTHIN, A MARKER FOR CANCER
; FILE REFERENCE: 21511/91057
; CURRENT RAPLICATION NUMBER: US/09/659,521
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: PCT/US99/05365
; PRIOR FILING DATE: 1998-03-11
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2442
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Pred. No. 3e-297;
0; Mismatches 1; Indels
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90; Conservative
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; LOCATION: (70)
US-09-659-521-1
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Matches 690;
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US-09-659-521-1
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                                                                          GATGTAGATGATAGATTTGAGACCCTGGAACTTGAAGTATCTCATGAAGAAACCGAGCAT
                                                                                                                                                    TCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGAAGAAGAAGATTGCACT
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CAAGAAGATGACCCCACAGAGAACCACAACAAGAGGATGATGAGTTTCTTATGGCGACT
                                                                                                                            AGTTACCACGTGGAAGAGACAGTTTCACAAGACTGTAATCAGGATATGGAAGAGATGATG
                                                                                                                                                                                                   TCTGAGCAGGAAAATCCAGATTCCAGTGAACCAGTAGTAGAAGATGAAAGATTGCACCAT
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Pan, Liqun
APPLICANT: Pan, Liqun
APPLICANT: Pan, Liqun
APPLICANT: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: LIQUAL APRICA
CURRENT FILING AND MERE: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
                                                                                                                                                                                                                                                                                                                                                                            AATGAAGGGATAGAAATCACAGAAGTAACTG 736
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Patent No. 6667154
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; ORGANISM: Homo sapiens
US-09-671-325-1791
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US-09-671-325-1791
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SEQ ID NO 1791
LENGTH: 2442
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Best Local S:
Matches 690
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US-09-49-016-16453/C

US-09-949-016-16453, Application US/09949016

Sequence 16453, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER,

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

SOFTWARE: FASTSEQ for Windows Version 4.0

SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                 Sequence 3447. Application US/09949016
| Sequence 3447. Application US/09949016
| Patent No. 681239
| GENERAL INFORMATION:
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WIMBER: US/09/949,016
| TITLE OF ILING DATE: 2000-10-20
| FRIOR APPLICATION NUMBER: 60/241,755
| PRIOR APPLICATION NUMBER: 60/237,768
| PRIOR PELING DATE: 2000-10-03
| PRIOR PELING DATE: 2000-10-03
| PRIOR PELING DATE: 2000-10-03
| PRIOR PELING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SEQ ID NO 3447
                                      29846 GATGAGTTTCTTATGGCGACTGATGTAGATGATAGATTTGAGACCCTGGAACCTGAAGTA 29787
       561 GATGAGTTTCTTATGGCGACTGATGTAGATGATAGATTTGAGACCCTGGAACCTGAAGTA 620
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4.9%; Score 115; DB 4; Length 95
Best Local Similarity 100.0%; Pred. No. 6.4e-45;
Matches 115; Conservative 0; Mismatches 0; Indels
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                                                                                                                               621 TCTCATGAAG 630
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ORGANISM: Human
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## Patent No. 6812339

## Fatent No. 6812339

## FARRAL INCRNATION:

## APPLICANT: VENTER, J. Craig et al.

## TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

## TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

## CURRENT APPLICATION NUMBER: US/09/949,016

## CURRENT APPLICATION NUMBER: 60/211,755

## PRIOR APPLICATION NUMBER: 60/211,768

## PRIOR APPLICATION NUMBER: 60/231,498

## PRIOR PELING DATE: 2000-10-03

## PRIOR APPLICATION NUMBER: 60/231,498

## PRIOR APPLICATION NUMBER: 60/231,498

## PRIOR PELING DATE: 2000-09-08

## PRIOR PELING DATE: D
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                                                                                                                                                                                                                                                                  346 ATTCAGTCCCTTCTCCATGAAATGGTACACGCAGAACATGTTGAGGGAGAAGACTTGCAA 405
                                                                                                                                                                                                                                                                                                                                                                                      466 GATGTAGATGATAGATTTGAGACCCTGGAACTTGAAGTATCTCATGAAGAAACCGAGCAT 525
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Best Local Similarity 100.0%; Pred. No. 3.9e-52;
Matches 130; Conservative 0; Mismatches 0;
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GRGANISM: Human

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(74730)

GOTHER INFORMATION: n = A,T,C or (18.09-949-016-13189)
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322 AAGTTTTATTAGG 334
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CRGANISM: Human
US-09-949-016-122345
US-09-949-016-122387
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; ORGANISM: Human
US-09-949-016-236
                                                                                                                                                                                                                                                                                                                                                  RESULT 16
US-09-949-016-236/c
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US-09-940-016-122387/c

i Sequence 122387, Application US/09949016

is fatent No. 6812339

i GENERAL INFORMATION:

i APPLICANTY VENTER, J. Craig et al.

i TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

i TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

if ILE REPERENCE: CLO1307

i CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

software: FaetSeq for Windows Version 4.0

i LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                  JERNERAL INFORMATION:
APPLICAMT: VENTER, J. Craig et al.
APPLICAMT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-0414
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRESEQ FOR WINDOWS VERSION 4.0
ILENGTH: 601
                                                                   1073 GGGAAAAATTGAGGAAGCAGTGAATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAG 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       696 GGGAAAAATTGAGGAAGCAGTGAATGCATTTAAAGAACTAGTACGCAAATACCCTCAGAG 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            425 AGAACCCCAGAATATCGAAGATGAAGCAAAAGAACAAATTCAGTCCCTTCTCCATGAAAT 484
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.3%; Score 77; DB 4; Length 601; Best Local Similarity 100.0%; Pred. No. 1.2e-26; Matches 77; Conservative 0; Mismatches 0; Indels
                        0; Indels
  Best Local Similarity 100.0%; Fred. No. 6e-32; Matches 88; Conservative 0; Mismatches
                                                                                                                                                               1133 TCCACGAGCAAGATATGGGAAGGCGCAG 1160
                                                                                                                                                                                                             636 rccaccaccadarardegaadececae 609
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; Sequence 122372, Application US/09949016
; Patent No. 6812339
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US-09-949-016-122372
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ORGANISM: Humar
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US-09-949-016-122345/c

US-09-949-016-122345, Application US/09949016

Bacquence 122345, Application US/09949016

Bacquence 122345, Application US/09949016

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHIGMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOOU307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR PAPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 122345

LENGTH: 601

LENGTH: 601

LENGTH: 601

SEQ ID NO 122345
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 236, Application US/09949016
; Sequence 236, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, U. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WOUNBER: US/09/949,016
; CURRENT APPLICATION NUMBER: US/02/941,755
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR PILING DATE: 2000-10-20
; PRIOR PILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 236
; LENGTH: 2208
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                                                                                                                           TGATGTGGATGATGCCA 321
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Length 601;
                                                                                                                               262 TAGGAAACTAGGAATCTATGATGCTGATGGTGATGGAGATTT
3.1%; Score 73; DB 4; Les 100.0%; Pred. No. 9.8e-25; tive 0; Mismatches 0;
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US-09-859-604-11/c

Sequence 11, Application US/09859604

Patent No. 6835370

GRNERAL INFORMATION:

APPLICANT: Wands, Jack R.

APPLICANT: Gela Monte, Suzanne M.

APPLICANT: Ghanbari, Hosein A.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS

FILE REFRENCE: 21466-032 CIP

CURRENT FILING DATE: 1999-11-08

CURRENT FILING DATE: 1999-11-08

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.1

FRIND 1.
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US-09-899-604-10/c
US-09-899-604-10/c
Sequence 10, Application US/09859604
Fatent No. 683530
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
APPLICANT: General, Hossein A.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REFERENCE: 21486-032 CIP
CURRENT FILING DATE: 2001-05-17
FRICK APPLICATION NUMBER: US/09/859,604
CURRENT FILING DATE: 1999-11-08
FILE REPERENCE: 2100-05-17
FRICK APPLICATION NUMBER: US/09/36,184
FRICK FILING DATE: 1999-11-08
SEQ ID NOS: 13
SEQ ID NO 10
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GOGANISM: Artificial Sequence

GOTHER INFORMATION: Description of Artificial Sequence:Location (-1)

GOTHER INFORMATION: oligonucleotide

(-1)
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) ORGANISM: Artificial Sequence
) FEATURE:
) OTHER INFORMATION: Description of Artificial Sequence:Location (-6)
) OTHER INFORMATION: oligonucleotide
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Query Match 0.9%; Score 21; DB 4; Length 1845; Best Local Similarity 100.0%; Pred. No. 9.6; Matches 21; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                          93 CAGCAGCGCTCCGGCAGCGG 113
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Factor No. 6499307
GENERAL INFORMATION:
FAPLICANT: PHILLIPS, M. IAN
FITLE OF INVENTION: MATHODS OF USE
FILE OF INVENTION: MATHODS OF USE
FILE OF INVENTION WHERE: USO-07-11
FILE OF INVENTION WHERE: USO-07-11
FRIOR FILING DATE: 1990-09-14
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19.69-494-016-13283

1 Sequence 13283, Application US/09949016

1 Patent No. 6812339

2 Geguence 13283, Application US/09949016

1 Sequence 13283, Application US/09949016

2 Geguence 13283, Application US/09949016

3 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPRENCE: CL001307

CURRENT APPLICATION NUMBER: 60/211,755

PRIOR FILING DATE: 2000-10-02

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 13283

LENGTH. 19984
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                                                                                                                               Length 601;
                           Ouery Match 1.9%; Score 45; DB 4; Length 601
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 45; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
NAME/KEX: misc_feature
LOCATION: (1828) .. (1828)
OTHER INFORMATION: WHERE N = A, T, C OR G
US-09-614-034-188
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ORGANISM: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13283
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Best Local
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43 GCAACAGCAGCAGCGGC 62

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jecquence 136, Application US/09949016
jecquence 136, Application US/09/096
jecquence 136, Application US/09/0949, Olf
jette Reference: CL001307
jette Reference: CL001307
jette Reference: CL001307
jette Reference: CL001307
jette Reference: CL000-04-14
jette Reference: CL000-04-14
jette Reference: Cl000-06-04-14
jette Reference: Cl000-10-20
jette Reference: Cl000-10-03
jette Refer
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APPLICANTION:
APPLICATION:
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                                                                                                                                                                   RESULT 24
US-09-489-0933/c
; Sequence 1933, Application US/09489039A
; Patent No. 6610836
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                                 157 dchácháchácháchácháchácháchách 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human
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US-09-949-016-3254
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| GENERAL INFORMATION: | GENERAL INFORMATION: |
| APPLICANT: Wands, Jack R. |
| APPLICANT: Deutch, Alan H |
| FILE REFERENCE: 2146-032 CIP |
| CURRENT APPLICATION NUMBER: US/09/859,604 |
| CURRENT FILING DATE: 1999-11-08 |
| PRIOR PILING DATE: 1999-11-08 |
| NUMBER OF SEQ ID NOS: 13 |
| SEQ ID NO 12 |
| LENGTH: 20 |
| LENGTH: 20 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence:Locations (-11); OTHER INFORMATION: Oligonucleotide
US-09-859-604-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 20;
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.9%; Score 20; DB 4; Best Local Similarity 100.0%; Pred. No. 29; Matches 20; Conservative 0; Mismatches (
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OTHER INFORMATION: score 15.600003814697
OTHER INFORMATION: seq LLLLLLSPWPWMA/HV
US-09-621-976-24
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Patent No. 6639063
                                                                                                                                                                                                                                                                            US-09-859-604-12/c
; Sequence 12, Application US/09859604
; Patent No. 6835370
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CGTGCAATGGCCCAGCGTAA 25
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                                                                                      20 cerecaareeccaeceraa 1
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ORGANISM: Artificial Sequence
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ORGANISM: Homo sapiens
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LOCATION: 109..186
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Best Local Similarity
Matches 20; Conserve
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US-09-621-976-24/c
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LENGTH: 342
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us-ys-ys-uc-lial, Application US/09949016
; Sequence 11878, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    TITLE OF INVENTION:
    TITLE OF INVENTION:
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REPERENCE: CLOO1307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14,755
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-010-03
; PRIOR FILING DATE: 2000-09-08
; SEQ ID NOS: 207012
; SEQ ID NO 11878
; LENGTHA LIA668
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Patent No. 681239
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILLS OF INVENTION WINBER:
60/241,755
FRIOR FILLNG DATE:
2000-10-20
PRIOR PILLNG DATE:
2000-10-03
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.9%; Score 20; DB 4; Length 8841; Best Local Similarity 100.0%; Pred. No. 29; Matches 20; Conservative 0; Mismatches 0; Indels
         CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION WUMBER: 60/24,755
PRIOR APPLICATION WUMBER: 60/237,768
PRIOR APPLICATION WUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ for Windows Version 4.0
LENGTH: 8841
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; ORGANISM: Human
US-09-949-016-14996
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ORGANISM: Human
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US-09-949-016-13554
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| Sequence 1812, Application US/09949016
| Sequence 1812, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| TYPLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERRACE: CLOO1307
| CURRENT APPLICATION NUMBER: US/09/949,016
| CURRENT APPLICATION NUMBER: 60/241,755
| PRIOR APPLICATION NUMBER: 60/241,755
| PRIOR APPLICATION NUMBER: 60/241,755
| PRIOR APPLICATION NUMBER: 60/231,498
| PRIOR PPLING DATE: 2000-10-03
| PRIOR PPLING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 2000-09-08
| NUMBER OF SEQ ID NOS: 2000-09-08
| SEQ ID NO 1812.
| LENGTH 1116
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REPERBNCE: CLOO1307
CURRENT APPLICATION WUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-09
RIOR PILING DATE: 2000-09-09
RIOR PILING DATE: 2000-09-09
SEQ ID NOS: 207012
SOFTWARE: FastESQ for Windows Version 4.0
SEQ ID NO 3254
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
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100.0%; Pred. No. 29;
tive 0; Mismatches 0; Indels
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O.9%; Score 20; DB 4;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches
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Patent No. 6812339
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Best Local Similarity 100.C
Matches 20; Conservative
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; ORGANISM: Human
US-09-949-016-3254
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ORGANISM: Human
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US-09-949-016-14996
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0.9%;
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Best Local Similarity 100.0
Matches 20; Conservative
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US-09-513-999C-35281
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Best Local Similarity
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                       ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12762
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    LENGTH: 117937
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-04-02

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRAEESEQ FOR Windows Version 4.0

SEQ ID NO 17029
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTON: POLYNORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTON: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASESEQ FOR WINDOWS VERSION 4.0

SEQ ID NO 12762
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29;
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SUTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13354
LENGTH: 11713
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100.0%; Pred. No.
tive 0; Mismatch
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; Sequence 17029, Application US/09949016
; Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                   43 GCAACAGCAGCAGCAGCGGC 62
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Best Local Similarity
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                                                                                                                                     TYPE: DNA
ORGANISM: Human
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US-09-949-016-17029
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SERVERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-1,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

SPRIOR PILING DATE: 2000-10-03

SPRIOR PILING DATE: 2000-10-03

SPRIOR PILING DATE: 2000-10-03

SROFWARE: FastSEQ for Windows Version 4.0

SEQ ID NOS: 207012
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Sequence 35281, Application US/09513999C

Parent No. 6783961

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PAPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PAPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PARENT FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 35281

LENGTH: 148
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88;
                                                                 0; Indels
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                                                                 0; Mismatches
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100.0%; Pred. No.
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US-09-949-10-1792/C
1 Sequence 1792, Application US/09949016
1 Sequence 1792, Application US/09949016
2 Patent No. 6812339
3 GENERAL INFORMATION:
3 APPLICANT: VENTER, J. Craig et al.
3 APPLICANT: VENTER, J. Craig et al.
3 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
3 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
4 TITLE OF INVENTION: WITH HUWAN DISEASE, METHODS OF DETECTION AND USES THEREOF
5 FILE REFERENCE: CLO01307
6 CURRENT FILING DATE: 2000-04-14
7 FRIOR FILING DATE: 2000-10-20
7 FRIOR APPLICATION NUMBER: 60/231,498
7 FRIOR FILING DATE: 2000-09-08
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0.8%; Score 19; DB 4; Length 1599;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 19; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 88;
Matches 19; Conservative 0; Mismatches 0; Indels
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(US-08-33,-214-25/C
; Sequence-25, Application US/08339214
; Patent No. 6348334
; GENERAL INFORMATION:
; APPLICANT: Nagata, Shigikazu
APPLICANT: Suda, Takashi
; APPLICANT: Takashi
; APPLICANT: Takashi, Tomoniro
; APPLICANT: Nakamura, No. 634833410
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; ORGANISM: Human
US-09-949-016-1792
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US-09-248-7964-13462/c

i Sequence 13462, Application US/09248796A

patent No. 6747137

i GENERAL INFORMATION:

I TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN:

I TILLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

I TILLE OF INVENTION: NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US/09/248,796A

PRIOR APPLICATION NUMBER: US/09/248,796A

PRIOR APPLICATION NUMBER: US/09/248,725

PRIOR PRILING DATE: 1999-02-13

PRIOR PILING DATE: 1999-08-13

PRIOR PILING DATE: 1999-08-13

NUMBER OF SEQ ID NOS: 28208

LENGTH: 309
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US-09-949-016-61822/C
is Sequence 6.1822, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT VENTER, J. Craig et al.
    TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
    CURRENT FILING DATE: 2000-04-14
    PRIOR PLILORATION NUMBER: 60/231,768
    PRIOR PLILOR DATE: 2000-10-20
    PRIOR PLILOR DATE: 2000-10-03
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     0; Mismatches
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     Matches 19; Conservative
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BARLIER APPLICATION NUMBER: 60/047,615
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,315
FILING DATE: 1997-04-11
                                                                                                                                 EARLIER APPLICATION NUMBER: 60/047,600 EARLIER FILING DATE: 1997-05-23 EARLIER APPLICATION NUMBER: 60/047,615 EARLIER FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,671
                                                          FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,618
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APPLICATION NUMBER: 60/047,581
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APPLICATION NUMBER: 60/047,598
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APPLICATION NUMBER: 60/047,582
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APPLICATION NUMBER: 60/047,596
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APPLICATION NUMBER: 60/047,632
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FILING DATE: 1997-05-23
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                                     60/040,336
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APPLICATION NUMBER: 60/047,503
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APPLICATION NUMBER: 60/047,584
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APPLICATION NUMBER: 60/047,587
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                                                                                                            ILING DATE: 1997-03-07
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APPLICATION NUMBER: 60
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APPLICATION NUMBER: 60
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TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA TITLE OF INVENTION: Encoding the Same NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS: 103
CORRESPONDENCE ADDRESS: ADDRESSE: Birch, Stewart, Kolasch & Birch STREET: P.O. Box 747
CITY: File Church STREET: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IMP PC COMPATA: MEDIUM TYPE: Floppy disk COMPUTER: IMP PC COMPATA: MEDIUM TYPE: Relabel Floppy SOFTWARE: PREADABLE FORM: WEDIUM TYPE: USOS/MS-DOS SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA: RAPLICATION NUMBER: US/08/339,214
FILING DATE: 10-NOV-1994
CLASSIFICATION 1435
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100.0%; Pred. No. 88;
iive 0; Mismatches 0; Indels
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER RILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
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LOCATION: 74..907
OTHER INFORMATION: /label= Figs_2-3
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APPLICATION NUMBER: 60/040,626
FILING DATE: 1997-03-07
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18-09-149-476-110/c
Sequence 110, Application US/09149476
Patent No. 6420526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MULPDY JI., Gerald M.
REGISTRATION UNMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110
TELECOMUNICATION INFORMATION:
TELECHONE: 703-205-8050
TELEFRAX: 703-205-8050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1623 base pairs
TYPE: nucleic acid
STRANDEDNESS: not releva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.8
Best Local Similarity 100.
Matches 19; Conservative
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ORIGINAL SOURCE:
ORGANISM: rat
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Page 19

RR PELICATION NUMBER: 60/056,886

RR FILING DATE: 1997-06-06

RR APPLICATION NUMBER: 60/056,886

R FILING DATE: 1997-08-22

RR APPLICATION NUMBER: 60/056,899

RR PILING DATE: 1997-08-22

RR APPLICATION NUMBER: 60/056,899

RR FILING DATE: 1997-08-22

RR APPLICATION NUMBER: 60/056,892

RR FILING DATE: 1997-08-22

RR APPLICATION NUMBER: 60/056,893

RR FILING DATE: 1997-08-22

RR APPLICATION NUMBER: 60/056,893

RR FILING DATE: 1997-08-22

RR APPLICATION NUMBER: 60/056,894

RR FILING DATE: 1997-08-22

RR APPLICATION NUMBER: 60/056,895

RR FILING DATE: 1997-08-22

RR APPLICATION NUMBER: 60/056,995

RR FILING DATE: 1997-08-22

RR F ER APPLICATION NUMBER: 60/047, 585

RR FILING DATE: 1997-05-23

RR PLICATION NUMBER: 60/047, 589

RR PLICATION NUMBER: 60/047, 589 PLING DATE: 1997-05-23

PILING DATE: 1997-05-23

APPLICATION NUMBER: 60(043,578

APPLICATION NUMBER: 60(043,578

APPLICATION NUMBER: 60(043,576 APPLICATION NUMBER: 60/047,588 FILING DATE: 1997-05-23 1997-05-23

Sequence 5583, Application US/09949016
| Sequence 5581, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT' VENTER, J. Craig et al. NOWN GENES ASSOCIATED
| TITLE OF INVENTION: POLYMORPHSMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| FILE REFERENCE: CLO01307
| CURRENT APPLICATION NUMBER: US/09/949,016
| CURRENT PILING DATE: 2000-04-14
| PRIOR FILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-03
| PRIOR PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-10-03
| PRIOR PRIOR FILING DATE: 2000-10-03
| PRIOR PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-10-03 ö Gaps ; 0 0.8%; Score 19; DB 4; Length 1821; llarity 100.0%; Pred. No. 88; Conservative 0; Mismatches 0; Indels DB 3; Length 1751; 88; 0; Indels Query Match 0.8%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 88; Matches 19; Conservative 0; Mismatches EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047, 501
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-08-25
EARLIER FILING DATE: 1997-08-25
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 891
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 891
EARLIER FILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-09-05
EARLIE 1836 AAAGGICTCTTCCTGCCTG 1854 692 AAAGGTCTCTTCCTGCCTG 674 Query Match Best Local Similarity Matches 19; Conserv TYPE:DNA CORGANISM: Human US-09-949-016-5583 RESULT 41 US-09-949-016-5583 ò

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Gaps

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APPLICATION NUMBER: 60/047,500 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,587 APPLICATION NUMBER: 60/047,492 APPLICATION NUMBER: 60/047,492
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
FILING DATE: 1997-03-07
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APPLICATION NUMBER: 60/047,615
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,618
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APPLICATION NUMBER: 60/047,598
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APPLICATION NUMBER: 60/047,613
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APPLICATION NUMBER: 60/047,612
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APPLICATION NUMBER: 60/043,580
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APPLICATION NUMBER: 60/043,568
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APPLICATION NUMBER: 60/043,569
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APPLICATION NUMBER: 60/043,312
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APPLICATION NUMBER: 60/043,313
                                      FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,334
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APPLICATION NUMBER: 60/047,597
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APPLICATION NUMBER: 60/047,633
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APPLICATION NUMBER: 60/047,592
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APPLICATION NUMBER: 60/047,584
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                                                                                   FILING DATE: 1997-03-07
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FILING DATE: 1997-05-23
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                  APPLICATION NUMBER:
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Pred. No. 88;
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APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: 784CIP2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 264, Application US/09149476
| Patent No. 6420526
| GENERAL INFORMATION:
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: 186 Human Secreted proteins |
| FILE REFERENCE: PZ00201 |
| CURRENT APPLICATION NUMBER: US/09/149,476 |
| CURRENT PILING DATE: 1998-09-08 |
| EARLIER APPLICATION NUMBER: PCT/US98/04493 |
| EARLIER APPLICATION NUMBER: 60/040,162 |
| EARLIER APPLICATION NUMBER: 60/040,163 |
| EARLIER PILING DATE: 1997-03-07 |
| EARLIER PILING DATE: 1997-03-07 |
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100.0%; Pred. No. cc...
0; Mismatches
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                                                                                              RESULT 42
US-09-620-312D-49/C
; Sequence 49, Application US/09620312D
""-" NO. 6569662
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                                        437 AGCAGCGCCACACACACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 49
LENGTH: 2286
36 AGCAGCGCCAACAGCAGCA 54
                                                                                                                                                                                                                                                                                                                                                                                                               Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
Ma, Yunging
Wang, Dunrui
Wang, Zhiwei
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Best Local Similarity 100.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                           Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
                                                                                                                                                                                                               APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
                                                                                                                                                                                                                                                                                                       Ren, Feiyan
                                                                                                                                                                                                                                                                                                                                                                        Wehrman, Tor
Xue, Aidong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: (69)..(1727)
US-09-620-312D-49
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EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-23
EARLIER FILING DATE: 1997-08-2
ER FILING DATE: 1997-04-11

ER PAPPLICATION NUMBER: 60/043, 672

ER PILING DATE: 1997-04-11

ER APPLICATION NUMBER: 60/043, 315

ER FILING DATE: 1997-04-11

ER FILING DATE: 1997-06-16

ER FILING DATE: 1997-06-16

ER FILING DATE: 1997-06-16

ER FILING DATE: 1997-06-26

ER FILING DATE: 1997-06-22

ER APPLICATION NUMBER: 60/056, 889

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056, 893

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056, 830

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056, 630

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056, 630

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056, 630

ER FILING DATE: 1997-08-22

ER RELING DATE: 1997-08-22

ER RELING DATE: 1997-08-22

ER RELING DATE: 1997-08-22

ER RELING DATE: 1997-08-22

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056, 662

ER FILING DATE: 1997-08-22

ER FILING DATE: 1997-08-22
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us-vy-yay-ulo-2642, Application US/09949016
; Sequence 2642, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT FILING DATE: 2000-04-14
; FRIOR APPLICATION NUMBER: 60/231,756
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR APPLICATION NUMBER: 60/231,498
; RINGRAPH FEASTSC for Windows Version 4.0
; SEQ ID NO 2642
; SEQ ID NO 2642
; TYPE: DNA
; ORGANISM: Human
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88;
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EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05.3
EARLIER FILING DATE: 1997-05.3
EARLIER FILING DATE: 1997-04.11
EARLIER FILING DATE: 1997-06.22
EARLIER FILING DATE: 1997-08.22
EARLIER FILING DATE: 1997-09.05
EARLIER FILING DATE: 1997
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US-09-949-016-2642
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Sequence 14384, Application US/09949016

Sequence 14384, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REPERENCE: CLOO1307

CURRENT PELLING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOCTWARE: PASELSE (or Windows Version 4.0)

SEQ ID NO 14384
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PAGUENER NO. 681239

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AL
FILE REFERENCE: CLOO1307;
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PELLING DATE: 2000-10-20

PRIOR PELLING DATE: 2000-10-03

PRIOR PELLING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PELLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE FELLING DATE: 2000-09-08

LENGTH: 7460
                0.8%; Score 19; DB 4; Length 6625; liarity 100.0%; Pred. No. 87; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 87;
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Matches 19; Conserva
                                                         Best Local Similarity
Matches 19; Conserv
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Best Local Similarity
Matches 19; Conserv
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ORGANISM: Human
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                                   Query Match
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US-09-949-016-633
US-09-949-016-633
Sequence 633, Application US/09949016
Patent No. 681239
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT PAPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTHARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 633
LENGTH: 3482
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PRIOR FILING DATE: 2000-09-99

CURRENT FILING DATE: 2000-09-99

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELICATION NUMBER: 60/231,768

PRIOR PELICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03
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                                                             Length 3462;
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88;
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                                                         Score 19; DB 4;
Pred. No. 88;
                                                         0.8%; Score 19; DB ilarity 100.0%; Pred. No. 88; Conservative 0; Mismatches
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LOCATION: (1)...(3482)
COTHER INFORMATION: n = A,T,C or G
US-09-949-016-633
                                                         Query Match
Best Local Similarity
Matches 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human
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US-09-949-016-2642
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RESULT 52

US-09-949-016-14588/c

is Sequence 14588, Application US/09949016

patent No. 6812339

is GENERAL INFORMATION

TITLE OF INVENTION: WITH HOWAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HOWAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION WINDER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR PAPLICATION NUMBER: 60/231,768

PRIOR PRILOR DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 14588

LEMCTH: 302604

MADER OF SEQ ID NOS: 207012

SEQ ID NO 14588
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86;
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Best Local Similarity 100.0%; Pred. No. 86;
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18759 AGCAGCGCAACAGCAGCA 18777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
; LOCATION: (1)...(300598)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11868
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; LOCATION: (1)...(302604)
; CTHER INFORMATION: n = A,T,C or G
US-09-949-016-14588
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
FEATURE:
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ORGANISM: Human
                                                                     RESULT 51
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                                                                                                      Sequence 15619, Application US/09949016

patent No. 6812339

j GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PEDICATION NUMBER: 60/231,768

PRIOR PEDICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-30

PRIOR PEDICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 15619

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Ouery 100.0%; Pred. No. 87;

Matches 19; Conservative O; Mismatches O; Indels
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   1777 CTTTAGAAAGAAACTGGAA 1795
                              4966 CTTTAGAAGAACTGGAA 4984
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US-09-949-016-17325
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LOCATION: (1)...(28843)
                                                                                  RESULT 49
US-09-949-016-15619
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15619
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ORGANISM: Human
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36 AGCAGCGGCAACAGCAGCA 54

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TYPE: DNA
ORGANISM: Human
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                                                                                                                                                                                                                                                 APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 14589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JERNERAL INPORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR PLILNG DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRESEQ FOR WINDOWS Version 4.0

SEQ ID NO 17119

LENGTH: 308362
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Gaps
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0; Indels
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  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.8%; Score 19; DB
100.0%; Pred. No. 86;
iive 0; Mismatches
                                                                                                                                                                                                        . Sequence 14589, Application US/09949016 ; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-949-016-17119/c
; Sequence 17119, Application US/09949016
; Patent No. 6812339
                                                                                         299448 GGGGAAAATTGAGGAAGC 299430
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                                                1072 GGGGAAAATTGAGGAAGC 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
| LOCATION: (1)...(302664)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14589
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// LOCATION: (1)...(308362)

OTHER INFORMATION: n = A,T,C or G

US-09-949-016-17119
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  Matches 19; Conservative
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Matches 19; Conserv
                                                                                                                                                               RESULT 53
US-09-949-016-14589/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Human
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Sequence 12777/C

Sequence 12777/A

Sequence 1277/A

Sequence 127/A

Sequence 127/
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APPLICANT: Wands, Jack R.

APPLICANT: Wands, Jack R.

APPLICANT: Genetch, Alan H

APPLICANT: Genetch Indenosis, 1000-05-17

FILE REPERENCE: 2146-032 CIP

CURRENT APPLICATION NUMBER: US/09/859,604

CURRENT FILING DATE: 1999-11-08

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 13

LENGTH: 22
                                                                                                     Gaps
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     Length 308362;
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US-09-859-604-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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          4,
Query Match

0.8%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 86;
Matches 19; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                  299264 GGGGAAAATTGAGGAAGC 299246
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Patent No. 6835370
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CCATION: (1)...(828152)

OTHER INFORMATION: n = A,T,C or G
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US-09-513-999C-10601

US-09-513-999C-10601

Sequence 10601, Application US/09513999C

Patent No. 6783961

GENERAL INFORMATION:

APPLICANT: Duclert, A.

APPLICANT: Duclert, A.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

TITLE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT APPLICATION NUMBER: US/06/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SEQ ID NO 10601

LEMCTH: 452

TURENTH: 452

TURENTH: 452

TURENTH: 452

TURENTH: 452
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US-09-270-767-10408
; Sequence 10408, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TILE OF INVENTION:
; FILE REFERENCE: File Reference: 7326-094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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CLASSIFICATION: 514

PRIOR APPLICATION DATA
APPLICATION NUMBER: FR 94-07191
FILING DATE: 13-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REGISTRATION NUMBER: 017753-058
TELECOMMUNICATION INFORMATION:
TELEPAX: (703) 836-620
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERSTICS:
SEQUENCE CHARACTERSTICS:
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1 LOCATION: 440

US-09-513-999C-10601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-482-842B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 319 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ORGANISM: Homo sapiens
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APPLICANT: KOMAN, Ahmet

APPLICANT: KOMAN, Ahmet

APPLICANT: CHASSIN, Dorine

APPLICANT: BELLET, Dominique

TITLE OF INVENTION: NEW PROTEIN CALLED EPIL/PLACENTIN,

TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF THIS PROTEIN AND

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION CONTAINING SUCH, DNA CODING FOR TITLE OF INVENTION: SAID PROTEIN

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: BUTNS, Doane, Swecker & Mathis

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

CONTAINED. TITLE

CONTAINED. TITLE
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APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradey K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 US
CURRENT PELICAN NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SEQ ID NO 3024
LENGTH: 286
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                      Score 18; DB 4; Length 22;
Pred. No. 2.76+02;
O; Indels
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COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: RC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/482,842B
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | FBATURE: | NAME/KEY: misc feature | O'NO. 6476212 700282183H1 | O'NHER INFORMATION: Incyte ID No. 6476212 700282183H1 | O'NHER INFORMATION: 87, 108, 146, 200, 239 | O'THER INFORMATION: a, t, c, g, or other US-09-313-294A-3024
                                                Query Match 0.8%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 2.7 Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3024, Application US/09313294A Patent No. 6476212 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08482842B
Patent No. 5910480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 CAACAGCAGCAGCAG 198
                                                                                                                                                                                                                         5 TGCAATGGCCCAGCGTAA 22
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                                                                                                                                                                             8 TGCAATGGCCCAGCGTAA 25
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ORGANISM: Zea mays
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US-09-313-294A-3024
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Sequence 36982, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPRENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 36982
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 40425/Application US/09949016

j Sequence 40425, Application US/09949016

j Barent No. 6812339

j GENERAL INFORMATION:
    TITLE OF INVENTION:
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES:
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES: 2000-04-14

CURRENT APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-06

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 40425

LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.8%; Score 18; DB 4; Length 601; Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 18; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.7e+02;
lve 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. ...
Marcheg 18; Conservative 0; Mismatches
                                2100 AAGGAAGGCTGCAAGATT 2117
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US-09-949-016-40425
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                                                                                                                                                                                                                                                           Query Match 0.8%; Score 18; DB 4; Length 529; Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%; Score 18; DB 4; Length 557;
100.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 0; Indels
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENSET. 054PRZ
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 16896
LENGTH: 561
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0.8%; Score 18; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09918686
Patent No. 6475739
GENERAL INFORMATION:
APPLICANT: Brunkow, Mary
APPLICANT: Brunkow, Mary
APPLICANT: Paeper, Bryan
APPLICANT: Paeper, Bryan
APPLICANT: Reaching-Hampton, Karen
TITLE OF INVENTION: GENOMIC DELETIONS
FILE REFERENCE: 240083.515
CURRENT APPLICATION NUMBER: US/09/918,686
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 557
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SEQ ID NO 10408
LENGTH: 529
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; Patent No. 6639063
                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-10408
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                                                                                                                                                                                                                                                                                                                                                                    43 GCAACAGCAGCAGCG 60
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Matches 18; Conservative
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ORGANISM: Homo sapiens

US-09-621-976-16896
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patent 42138, Application US/09949016

Sadence 42138, Application US/09949016

Patent No. 6812339

GENERAL INPORMATION

APPLICANT: VENTER, J. Craig et al.

TILLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TILLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-037,768

PRIOR FILING DATE: 2000-10-037,768
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US-09-949-016-42139
US-09-949-016-42139, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL0001307
APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-09

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NOS: 207012

SEQ ID NO 42137

LENGTH. 6013
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0.8%; Score 18; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 601;
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222 ATGATGCTGATGGTGATG 239
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; ORGANISM: Human
US-09-949-016-42137
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; ORGANISM: Human
US-09-949-016-42138
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US-09-949-016-42138
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| Sequence 42136, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| TITLE OF INVENTION:
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| CURRENT FILING DATE: 2000-04-14
| FRIOR FILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SOFTWARE: RaseEEQ for Windows Version 4.0
| SEQ ID NO 42136
                                            GENERAL INFORMATION:

FACEDATOR AT 135

SEQUENCE 42135

GENERAL INFORMATION:

FALEL OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE: CLOOL307

CURRENT FILING DATE: 2000-04-14

FRICK APPLICATION NUMBER: 05/241,755

FRICK APPLICATION NUMBER: 60/241,755

FRICK APPLICATION NUMBER: 60/241,768

FRICK PILING DATE: 2000-10-20

FRICK PILING DATE: 2000-10-03

FRICK PILING DATE: 2000-10-03

FRICK PILING DATE: 2000-10-03

FRICK PILING DATE: 2000-10-03

FRICK PILING DATE: 2000-09-08

FRICK PILING DATE
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US-09-949-016-42137
Sequence 42137, Application US/09949016
; Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-42135
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US-09-949-016-42136
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US-09-949-016-42136
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-53139
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US-09-949-016-67303
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| Sequence 42140, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| CURRENT APPLICATION NUMBER: US/09/949,016
| CURRENT PILING DATE: 2000-04-14
| PRIOR APPLICATION NUMBER: 60/241,755
| PRIOR PILING DATE: 2000-10-03
| PRIOR PLING DATE: 2000-10-03
| PRIOR PLING DATE: 2000-10-03
| PRIOR PLING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SOCTHARE: FBSESEQ for Windows Version 4.0
| LENGTH: 601
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Sequence 53139, Application US/09949016

Sequence 53139, Application US/09949016

Patent No. 6812339;
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768
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100.0%; Pred. No. 2.7e+02;
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0.8%; Score 18; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0;
                   CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-33

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-00-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 601
CURRENT APPLICATION NUMBER: US/09/949,016
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Matches 18; Conserva
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; ORGANISM: Human
US-09-949-016-42139
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| FGRENEAL INFORMATION:
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| JAPPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF:
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| CURRENT FILING DATE: 2000-04-14
| PRIOR PELLING DATE: 2000-10-20
| PRIOR PELLING DATE: 2000-10-03
| PRIOR APPLICATION NUMBER: 60/231,768
| PRIOR APPLICATION NUMBER: 60/231,498
| PRIOR FILING DATE: 2000-10-03
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Sequence 69417, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 05/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASELSEQ for Windows Version 4.0
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100.0%; Pred. No. 2.7e+02;
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Best Local Similarity 100.0%; Pred. No. ...
Matches 18; Conservative 0; Mismatches
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 53139
LENGTH: 601
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, Patent No. 6812339
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GENERAL INFORMATION:

FILE OF INVENTION:

TITLE OF INVENTION:

TILING DATE: 2000-04-14

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

SEQ ID NOS: 207012

SEQ ID NO 69418

LENGTH: 601
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105-09-349-016-69419/C

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; SEQ ID NO 69417
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-69417
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; ORGANISM: Human
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Query Match 0.8%; Score 18; DB 4; Length 601
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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